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LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Virginia
                                                                                                                                                                                                                                                        RESULT 1
US-08-241-054-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: V
COUNTRY:
Sequence 50, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 30, Appl
Sequence 50, Appl
Sequence 5, Appli
Sequence 76, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149, App
10, Appl
29, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
3, App
4, App
2, App
                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      November 14, 2004, 13:32:59; Search time 27 Seconds (without alignments) 34.387 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-241-054-59
US-08-390-156A-14
US-08-390-156A-22
US-08-439-817-30
US-08-439-817-30
US-08-485-508-34
US-08-241-054-5
US-08-391-156A-76
US-08-39-817-4
US-08-439-817-4
US-08-439-817-4
US-09-428-082B-149
US-08-444-818-554
US-08-444-818-554
US-08-161-705-76
US-08-161-705-76
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US-08-161-705-76
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US-09-171-705-76
US-08-617-929-24
US-08-388-852B-6
                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-241-054-100
US-08-241-054-117
                                                                                                                                                                                                 478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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71
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Match Length
                                                                                                                                                                                                                                           seq length: 0
seq length: 14
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                                                                                                                                Perfect score:
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Maximum DB
                                                    OM protein
                                                                                                                                            Sequence:
                                                                                                                                                                                                 Searched:
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                                                                          Run on:
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No.
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28 24 33.8 12 1 US-08-390-156A-64 Sequence 10, Appl 29 24 33.8 12 1 US-08-390-156A-64 Sequence 64; Appl 31 24 33.8 12 1 US-08-390-156A-88 Sequence 64; Appl 32 24 33.8 12 1 US-08-390-156A-103 Sequence 103, Appl 32 24 33.8 12 1 US-08-439-817-6 Sequence 103, Appl 34 24 33.8 12 1 US-08-439-817-80 Sequence 66, Appl 35 24 33.8 12 1 US-08-439-817-99 Sequence 20, Appl 36 24 33.8 12 1 US-08-439-817-209 Sequence 20, Appl 36 24 33.8 12 1 US-08-485-508-68 Sequence 20, Appl 39 24 33.8 12 1 US-08-485-508-100 Sequence 100, Appl 40 24 33.8 12 1 US-08-485-508-100 Sequence 110, Appl 41 24 33.8 12 1 US-08-485-508-110 Sequence 27, Appl 41 24 33.8 12 1 US-08-485-508-100 Sequence 27, Appl 42 24 33.8 12 1 US-08-481-908-27 Sequence 27, Appl 44 24 33.8 12 1 US-08-410-908-27 Sequence 5, Appl 44 24 33.8 12 1 US-08-109-27 Sequence 5, Appl 44 24 33.8 12 1 US-08-109-27 Sequence 27, Appl 44 24 33.8 12 1 US-08-117-869-5 Sequence 27, Appl 44 24 33.8 12 1 US-08-117-869-5 Sequence 27, Appl 44 24 33.8 12 1 US-08-117-869-5 Sequence 27, Appl 44 24 33.8 12 US-08-128-1109 Sequence 110, Appl 45 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 45 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 46 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 47 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 47 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 47 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 48 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 49 24 33.8 12 US-08-110-908-208-28-38-38 Sequence 110, Appl 49 24 33.8 12 US-08-110-908-27 Sequence 110, Appl 54 24 33.8 12 US-0
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## ALIGNM

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GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Martens, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: CWITLA, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Elam-1
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppdidisk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US (08/057,295
PILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
PILING DATE: 06-MAY-1992
ATONNEY/AGENT INFORMATION:
NAME: SWISS, GEXALD F
REGISTRATION NUMBER: 30,113
REFERENCE/POCKET UNMBER: 1023.1A
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.4%; Score 28; DB 1; I 66.7%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Affymax Technologies, N.V. STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
                                                                                                             ; Sequence 14, Application US/08390156A; Patent No. 5648458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 4; Conserv
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                                                                                             US-08-390-156A-14
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                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cavita, Steven E.
APPLICANT: Cavita, Steven E.
APPLICANT: Coller, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland Fritsch, Beatrice
TITLE OF INVENTION: Selectins Including Endothellum Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.4%; Score 28; DB 1; I Best Local Similarity 50.0%; Pred. No. 1.3e+02; Matches 4; Conservative 3; Mismatches 1;
                                                                                           Score 28; DB 1; Pred. No. 1.3e+02; 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Burne, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia COUNTRY: USA COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000324-002
                                                                                                                                                                                                                                                                                                                                  Sequence 50, Application US/08241054 Patent No. 5643873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 50:
SEGUIENCE CHARACTERISTICS:
LENGTH: 12 amino acide
                                                                                           39.4%;
                                                                                      Query Match
Best Local Similarity 66.7
Matches 4; Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-34
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-241-054-50
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Gaps

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IndelB

Length 12;

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APPLICANT: Cwirls, Steven E.
APPLICANT: Cwirls, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Ruhland-Fritsch, Beatrice
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.4%; Score 28; DB 1; 66.7%; Pred. No. 1.3e+02
                                                                                                                                                                                                                                                                                                                                                                                           000324-046/1056.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
PRIOR APPLICATION NUMBER: US 07/881,395
ATTOCHARY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERNICE/DOCKET NUMBER: 36,691
REFERNICE/DOCKET NUMBER: 36,691
TELEPHONE: 415,496-2300
                                             UMBER: US/08/439,817
12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
IOR APPLIANCE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/08439817
Patent No. 5728802
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Techno
STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
Matches 4; Conserv
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                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304
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US-08-439-817-30
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STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT: Dower,
APPLICANT: Coller, Kerry o.
APPLICANT: Keller, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
""".R. OF INVENTION: Molecule I (ELAM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/081,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: SWIEST GENERAL OF:
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
TELEBRATION HOPPRATION:
TELEBRATION HOPPRATION:
TELEBRATION 1496-2300
TELEBRAX: 415-424-0832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.4%; Score 28; DB Best Local Similarity 50.0%; Pred. No. 1.3e Matches 4; Conservative 3; Mismatches
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-439-817-14
; Sequence 14, Application US/08439817
; Patent No. 5728802
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Cwirla, Steven E.
Dower, William J.
Koller, Kerry J.
                             : Affymax Technology 4001 Miranda Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                    Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 SIIWAMMO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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94304
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                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lee, Jung Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF SEQUENCES: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%; Score 28; DB 1; Length 12; 50.0%; Pred. No. 1.3e+02;
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COU
                                                                                                                                                                                                                                                                                                                                                                                       000324-046/1056.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 36,691
RELEPHONE: 415-496-2300
TELEPHONE: 415-496-2300
TELEPRX: 415-496-2300
TELEPRX: 415-424-0832
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARATTERISTICS:
LENGTH: 12 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08485508
Patent No. 5786322
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cwirla, Steven E. Dower, William J. Koller, Kerry J.
11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rss: single
linear
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MOLECULE TYPE: peptide

US-08-439-817-30
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5 NMLWNMMO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Boller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
APPLICANT: Ruhland-Fritsch, Beatrice
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 12;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 1; 1
Pred. No. 1.3e+02;
                                                                                                000324-002/1056
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REFERENCE/DOCKET NUMBER: 000324-002/1056
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054

FILING DATE: 11-MAY-1994

CLASSIPICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395

FILING DATE: 06-MAY-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Affymax Technologies, NV 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-485-508-50
; Sequence 50, Application US/08485508
Patent No. 5786322
; GENERAL INFORMATION:
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 06,691
REFRENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                           TELBEAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            99.4
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide US-08-485-508-34
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CITY: Palo Alto
STATE: California
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cancer; tumour; human; GAGE-1.

Homo sapiens.

Synthetic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-cells, Nc cells, LaK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of epithelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides and useful for delivering a'therapeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering cell adhesion to a biomaterial, for detecting tumoures, for detecting inflammation, for detecting a CD66 protein or its ligand, for altering anglogenesis by contacting endothelial cells, tumour cells or immune cells, for altering an immune response, and for altering keratinocyte proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 'polypeptides, and modulating immune cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ligands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one CD66 family polypeptide and/or at least one ligand of the polypeptide.
                                                                                            CD66; CEACAM, adhesion molecule, antiviral, antibacterial, antiinflammatory; cytostatic, neutrophil activation; proliferation; differentiation; cancer, anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.5%; Score 33; DB 4; Length 14; 60.0%; Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM73036 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                    25-AUG-2000, 2000WO-US023482.
                                                                                                                                                                                                                                                                                                                                                                                        99US-0150791P.
17-MAY-2001 (first entry)
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                                               CD66 peptide CD66f(11)-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skubitz APN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SLDASIIWAM 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SKUB/) SKUBITZ K M. (SKUB/) SKUBITZ A P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-234981/24.
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                                                                                                                                                                                                                                             WO200113937-A1.
                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999;
02-SEP-1999;
                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skubitz KM,
                                                                                                                                                                                                                                                                                            01-MAR-2001
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New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral infections, cancers and tumors.

Claim 1; SEQ ID NO 295; 357pp; English.

Liu Z;

Liu L,

Simard JJL, Diamond DC,

WPI; 2004-315564/29.

(MANN-) MANNKIND CORP

05-SEP-2003; 2003WO-US027706 06-SEP-2002; 2002US-0409123P

WO2004022709-A2

18-MAR-2004

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The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-33 amino acids (ESQ ID NO:108-610); (b) an epitope cluster comprising the polypeptide of (a); (c) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a)-(c); or (e) a nucleic acid encoding the polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and can be used in vaccines. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection; cancer; tumour; human; GAGE-1.
                                                                                                                                                                                       infections, cancers and tumours. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                        40.8%; Score 29; DB 8; Length 9; 50.0%; Pred. No. 1.7e+06; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GAGE-1 epitope SEQ ID NO:300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM73041 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0
Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MANN-) MANNKIND CORP
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                                                                                                                                                                                                                                                    Sequence 9 AA;
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The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope cluster comprising the polypeptide of (a); (C) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a)-(c); or (e) a nucleic acid encoding the polypeptide of (a)-(d). (1) has virucide and cytostatic activities, and can be used in vaccines. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of viral infections, cancers and tumours. The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection; cancer; tumour; human; GAGE-1.
                                                                       New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral infections, cancers and tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral infections, cancers and tumors.
                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 8; Lengtn y;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                           infections, cancers and tumours. The pres exemplification of the present invention.
               Liu Z;
                                                                                                                                Claim 1; SEQ ID NO 300; 357pp; English
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               Liu
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                                                                                                                                                                                                                                                                                                                                                                   40.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
               Diamond DC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diamond
                                                                                                                                                                                                                                                                                                                                                                                                                             7 IIWAMMON 14
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                                          WPI; 2004-315564/29
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ILWLLMNN
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               Simard JJL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM73042;
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The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-13 amino acids (SEQ ID NO:108-610); (b) an epitope cluster comprising the polypeptide of (a); (c) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a)-(c); or (e) a nucleic acid encoding the polypeptide of (a)-(c); or (b) a nucleic acid encoding the can be used in vaccines. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of viral
cluster comprising the polypeptide of (a); (c) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a) - (c); or (e) a nucleic acid encoding the polypeptide of (a) - (a). (I) has virucide and cytostatic activities, and can be used in vaccines. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of viral infections, cancers and tumours. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitope, epitope cluster, virucide, cytostatic, vaccine, viral infection, cancer; tumour, human, GAGE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral infections, cancers and tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GAGE-1 epitope SEQ ID NO:299.
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                                                                                                                                                                                                                                                                                                                                                                       ADM73040 standard; peptide; 10
                                                                                                                                                                                     40.8%;
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The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-33 amino acids (SEQ ID NO. 108-610); (b) an epitope

Claim 1; SEQ ID NO 301; 357pp; English.

Sequence 10 AA;

Length 10;

DB 8; 2e+02;

Score 29; Pred. No.

40.8%;

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Transforming growth factor inhibitory peptide P53.
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                                                               Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope cluster comprising the polypeptide of (a); (c) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a) - (c); or (e) a nucleic acid encoding the polypeptide of (a) - (d). (I) has virucide and cytostatic activities, and can be used in yaccines; The methods and compositions of the present invention are useful for the diagnosis and/or treatment of viral
                                                                                                                                                                       cluster; virucide; cytostatic; vaccine; viral infection;
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                                                                                                                                                                                                                                                                                                                                                  Liu Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 294; 357pp; English.
                                                                                                                                                   Human GAGE-1 epitope SEQ ID NO:294
                                                                                 ADM73035 standard; peptide; 10 AA.
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cancer; tumour; human; GAGE-1
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Hepatotropic, antagonist, transforming growth factor betal, IGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor, mimetope, cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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AAO14709
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## ALIGNMENTS

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Geneseq 23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Database

AAV	7 10000
ឧ	AAY93098 standard; peptide; 14 AA.
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AC	AAY93098;
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DE	Transforming growth factor inhibitory peptide P144.
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K	Hepatotropic; antagonist; transforming growth factor betal; TGF-bl
KW	competitive inhibition; collagen synthesis stimulation inhibit
KW	extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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02-JUN-2000.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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geneseqp20028:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\*

99WO-ES000375 23-NOV-1999; 98ES-00002465 24-NOV-1998;

Aay93098 Transform

(CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

WPI; 2000-411935/35.

Aay 29500 Transform
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AAW46010 AAY93095

AAW26865 AAW63875

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Disclosure; Page 31; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis 

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial anino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Borras Cuesta F;
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                                                                                                                                                Transforming growth factor inhibitory peptide P55.
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0.046;
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                   AAY93009 standard; peptide; 12
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                                                             Score 71; DB 3; Length 14; Pred. No. 1e-05;
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0; Mismatches
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
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                                                               Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Pred. No. 0.046;
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                                                                                                                                Disclosure; Page 27; 86pp; Spanish.
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75.0%;
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Pred. No. 0.046;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, specifically cirrhosis
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TSLDATMIWTMM 12
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Best Local Similarity
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Matches
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those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the juvention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
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Pred. No. 2.7;
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                                                                                                                                                                      disease, specifically cirrhosis
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Pred. No. 9.2;
1; Mismatches
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                                                                                                                                                                                                              AAY93010 standard; peptide; 12 AA.
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Conservative
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X MEDLINE=22404279; PubMed=12516573;

A Kurth J., Pernick A., Schmitz R., Tking-Konert C., Chiorazzi N.,

A Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;

"Lack of deleterious somatic mutations in the CD95 gene of plasmablasts from systemic lupus erythematosus patients and autoantibody-producing cell lines.";

E ENBL, D31968; BAA20850.1;

E EMBL, AJ279011; CAC35539.1;

E EMBL, AJ279012; CAC35539.1;

E EMBL, AJ279013; CAC35540.1;

E EMBL, AJ279013; CAC35540.1;

E EMBL, AJ279013; CAC35541.1;

E EMBL, AJ279014; CAC35541.1;

E EMBL, AJ279019; CAC48839.1;

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T SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;
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WEDLINE=92134256; PubMed=1734862;

Touhara K., Prestwich G.D.;

Touhara K., Prestwich G.D.;

"Binding site mapping of a photoaffinity-labeled juvenile hormone binding protein.";

Biochem. Biophys. Res. Commun: 182:466-473 (1992).

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SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.8%; Score 19; DB 2; Length 11; Best Local Similarity 57.1%; Pred. No. 1.4e+04; Matches 4; Conservative 2; Mismatches 1; Indels
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11 AA, 1071 MW, D232A98E705045BD CRC64;
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Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Muschen M., Wolf J., Hansmann M.L., Diehl V., Muschen M., Re D., Brauninger A., Wolf J., Hansmann M.L., Diehl V., Kuppers R., Rajewsky K.; Supers R., Rajewsky K.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=88003971; PubMed=2820677; Locke J., White B.N., Watt G.R.; Cloning and S. end nucleotide sequences of two juvenile hormone—inducible vitellogenin genes of the African migratory locust.";
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Bukaryota (Atazoma), Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha, Acridoidea, Acrididae, Oedipodinae, Locusta.
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Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
Nakanishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.8%; Score 19; DB 2; Length 10; 40.0%; Pred. No. 1.3e+04; Live 3; Mismatches 0; Indels
  Score 19; DB 2; Length 10;
Pred. No. 1.3e+04;
                                             1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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                                                5; Mismatches
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Locusta migratoria (Migratory locust)
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
05-UTL-2004 (TrEMBLrel. 27, Last anno
Fas antigen (CD95 antigen) (Fragment)
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EMBL; M17334; AAA29285.1; -.

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SEQUENCE 10 AA; 1116 MW;
    26.8%;
                        33.3%;
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1 MWALI 5
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                                                                                                                                            Gaps
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"Third instar cuticle proteins.";
submitracd (XXX-2000) to Swiss-Prot.
-!- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
FlyBase; FBgn0061208; Lcp2a.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MUN-2003 (TrEMBLrel. 24, Last annotation update)
Larval cuticle LCP2A protein (Minor band protein) (Fragment).
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Artropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechococcus sp. (strain PCC 6301) (Anacystis nidulans). Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBI_TaxID=1139;
                                                                                                Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.2%; Score 20; DB 2; Length 13; 66.7%; Pred. No. 1.1e+04;
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InterPro; IPR000618; Insect cuticle.
PROSITE; PS00233; CUTICLE; PARTIAL.
                                                                                           Score 21, DB 2; Length 14;
Pred. No. 7.5e+03;
3; Mismatches 1; Indels
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10 AA; 1100 MW; 9DCF320732C44DDA CRC64;
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                                                  0BC0478DE855A33B CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last amnotation update)
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STRAIN=OREGON-R; TISSUE=LARVA;
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EMBL; S58974; AAP13908.1; -.
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Matches 4; Conservative
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1 TSLESSYL 8
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2 TSLEAA 7
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Fetzner S., Muller R., Lingens F.,
"Purification and some properties of 2-halobenzoate 1,2-dioxygenase,
two-component enzyme system from Pseudomonas cepacia 2CBS.";
J. Bacteriol. 174:779-290(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Teleostei, Euteleostei, Neoteleostei, Cichlidae, Orecchromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98115113; PubMed=9649539;
MEDLINE=98115113; PubMed=9649539;
Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
Figueroa F., Sultmann H., Klein J.,
Linkage relationships and haplotype polymorphism among cichlid MHC
Genetics I B loci.";
Genetics 18 199:1527-1537(1998).
EMBL; AF050005; AAC41441.1; -.
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NON_TER 1.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholdería.
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Pred. No. 5.8e+03;
1; Mismatches 0; Indels
                                                                                                                                    29.6%; Score 21; DB 2; Length 10; 50.0%; Pred. No. 5.2e+03; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 12 (Fragment).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
2-HALOBENZOATE 1,2-dioxygenase component A beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;
                                                                                                  D88458DDDDDAB2CD CRC64;
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 chloroplasts.";
Arch. Biochem. Biophys. 316:572-584(1995)
PIR; S69159; S69159.
                                                                                                                                                                                                                                                                                                                                                                                        Created)
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873 MW;
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Best Local Similarity 75.v.,
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nes 4; Conservative
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Microbiology 141:3087-3093(1995).
Microbiology 141:3087-3093(1995).
--- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-
--- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-
terminal amino acid residues but not N-terminal blocked ones.
Optimum activity is measured at pH 7.5. May be important in the
nutrition and pathogenesis of the organism in the human oral
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Caryophyllales, Amaranthaceae, Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 33624;
MEDLINE=96118234; PubMed=8574402;
Spratt D.A., Greenman J., Schaffer A.G.;
"Capnocytophaga gingivalis aminopeptidase: a potential virulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- COFACTOR: Requires magnesium or calcium.
Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;
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Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
Flavobacteriaceae; Capnocytophaga.
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                                                                            Length 8;
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Cystathionine gamma synthase (Fragment).
Spinacia oleracea (Spinach)
                                   8 AA; 965 MW; FF9DC37B1046D876 CRC64;
                                                                        29.6%; Score 21; DB 2; I
80.0%; Pred. No. 1.8e+06;
.ive 0; Mismatches 1;
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Aminopeptidase (EC 3.4.11.-) (Fragment)
                                                                                                                                                                                                                                                                                         10 AA
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EMBL; AY128666; AAM96953.1; -.
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10 AA; 1306 MW;
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MEDLINE=22615572; PubMed=12729892;
Moreno M.U., San Jose G., Orbe J., Paramo J.A., Beloqui O., Diez J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Peter M., Mugneret F., Aurias A., Thomas G., Magdelenat H.,
Delattre O.;
"An EWS/ERG fusion with a truncated N-terminal domain of EWS in
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Pred. No. 3.7e+03;
3; Mismatches 0; Indels
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Pred. No. 4.8e+03;
1; Mismatches 3; Indels
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                                                                                                                 CBE97F0E53277362 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Flavocytochrome b-558 alpha polypeptide (Fragment).
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Last annotation update)
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Theor. Appl. Genet. 86:935-942(1993).
PIR; PQ0731; P00731.
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Int. J. Cancer 67:339-342(1996).
                                                                                                                                                                      31.0%;
40.0%;
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50.0%;
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                                                                                                              11 AA; 1319 MW;
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Query Match
Beet Local Similarity 40.vv.
Beet Local Similarity
2, Conservative
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1 ATVVW 5
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 12 (Fragment).
Orcochromis niloticus (Nulle tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Actinopterygii; Actinopterygii; Percomorpha; Perciformes; Labroidei; Cichlidae; Orecchromis.
                       Figure F., Sultmann H., Klein J.;
"Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci.":
EMBL; AF050004; AAC41343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=98115113; PubMed=9649539;
Malaga=Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
Malaga=Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
Figueroa F., Sulraman H., Kleżn J.;
"Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
Genetics 149:1527-1537(1998).

EMBL, AF050008; AAC41347.1; -.
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QYMIU2;
01-MAR-2004 (TERMELrel. 26, Created)
01-MAR-2004 (TERMELrel. 26, Last sequence update)
01-MAR-2004 (TERMELrel. 26, Last sequence update)
Unidentified 5.7/35K protein (Fragment).
Oryza sativa (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maiplantae; Streptophyta; Enbryophyta; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
NCBL_TAXID=4530;
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"A rice protein library; a data-file of rice proteins separated by
two-dimensional electrophoresis.";
     Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
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Pred. No. 3.7e+03;
1; Mismatches 0; Indels
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NON TER 11 11
SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
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75.0%;
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5 SIVW 8
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 12 (Fragment).
MHC class II B locus (Nie tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
NCBI_TaxID=8128;
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C3H/He;
MEDLINE=20127858; PubMed=10660538;
Munsch D., Watanabe-Pukunaga R., Bourdon J.C., Nagata S., May E.,
Yonish-Rouach E., Reisdorf P.;
"Human and mouse Ras (APD-1/CD95) death receptor genes each contain
p53-responsive element that is activated by p53 mutants unable to
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                          Q56972
Q71zi0
Q7zzi6
Q7zzi9
Q8adi8
Q7m348
Q7m350
Q7m351
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1242 MW; 22145E32CDC37043 CRC64;
                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                ALIGNMENTS
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. Biol. Chem. 275:3867-3872 (2000).

EMBL; AF282865; AAG02410.1; -.

GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                             Created)
         Q7ZZJZ
Q7ZJZ
Q78118
Q56972
Q7ZZIO
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MEDLINE=98315113; PubMed=9649539;
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Q9ESUS;
01-MAR-2001 (TEMBLEEL: 16,
01-MAR-2001 (TEMBLEEL: 16,
01-JUN-2003 (TEMBLEEL: 24,
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60.0%;
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IWAVL 8
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Q86410 homo sapien
Q86410 homo sapien
Q86410 homo sapien
Q7m1/3 spinacia ol
Q7m3/95 orecohromis
Q9756 burkholderi
Q84178 synechococc
P8238 drosophila
Q2536 locusta mig
Q9uel0 homo sapien
Q2536 locusta mig
Q9uex manduca sex
Q9twx few few sex
Q9twy few few sex in
Q9sdbb lepilemur sex
Q9tabb lepilemur sex
Q9tabb microcebus
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homo sapien
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                                                                           November 14, 2004, 13:17:28 ; Search time 122.5 Seconds (without alignments) 65.757 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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2: uniprot_trembl:*
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1 TSLDASIIWAMMQN 14
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Match Length DB
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Maximum DB seq length: 14
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Perfect score:
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Gaps

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alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (dadus sp.) (fragme C; Species: Gadus sp. (cod)
C; Species: Gadus sp. (cod)
C; Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C; Accession. S66199
R; Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.; FEBS Lett. 367, 237-240, 1995
A; Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
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A;Accession: S66195
A;Molecule type: protein
A;Residues: 1-6 <4JES
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase
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A;Reference number: PH1754; MUID:93301585; PMID:8391057
A;Accession: PH1768
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <POR>
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IG H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O2-Un-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession. PH1602
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 179, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic A;Reference number: PH1580; MUID:93301609; PMID:8315387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                processing enzyme, 33K - black gram (fragment)
C;Species: Vigna mungo (black gram)
C;Species: Vigna mungo (black gram)
C;Species: Vigna mungo (black gram)
C;Date: 14-Teb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66248
R;Okamoto, T.; Minamikawa, T.
Eur. J. Biochem. 231, 300-305, 1995
A;Title: Purification of a processing enzyme (VmPE-1) that is involved in post-translat A;Reference number: S66248; MUID:95361851; PMID:7635141
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C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH176
R;Porcelli, S; Yockey, C. E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
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A;Molecule type: DNA
A;Residues: 1-7 <VLI>
A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034
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                                                                                                             Query Match 26.8%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0;
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Pred. No. 2.8e+05;
1; Mismatches 1;
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Pred. No. 1.6e+03;
2; Mismatches 4;
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A;Residues: 1-7 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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60.0%;
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Best Local Similarity 33.3%;
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Best Local Similarity 60.0.
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1 DEGTRWAVL 9
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A,Molecule type: protein
A,Residues: 1-10 <OKA>
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2 ASSLW 6
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Antimicrob. Agents Chemother. 33, 1153-1159, 1989
Aritle: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant invo
A;Reference number: S09651; MUID:90024972; PMID:2552900
A;Accession: S09652
                                                                                                                                                                                                                                                                                                                                                      T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C; Accession: PH1709
R; Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A; Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
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A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A,Reference number: PT0509; MUID:91277601; PMID:1711558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%; Score 20; DB 2; Length 14; 40.0%; Pred. No. 1.5e+03; Ative 4; Mismatches 0; Indels
                                                             Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.8%; Score 19; DB 2; Length 6; 60.0%; Pred. No. 2.8e+05; tive 1; Mismatches 1; Indels
     A; Note: sequence extracted from NCBI backbone (NCBIP:75379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: PH1754; MUID: 93301585; PMID: 8391057
                                                        29.6%; Score 21; DB 2; I 50.0%; Pred. No. 9.6e+02; tive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Status: translation not shown
A/Status: translation not shown
A/Residues: 1-6 <FBE>
A/Experimental source: adult thymus, strain BALB/C
C/Keywords: T-cell receptor
                                                                                 Best Local Similarity 50.03
Matches 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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Matches 3, Conservative
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4 SMDSNYQLIW 13
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1 TSLESSYL 8
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <POR>
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J. Exp. Med. 1
                                                          Query Match
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C;Accession: 164829
R;Boles, D.J.; Proia, R.L.
R;Boles, D.J.; Proia, R.L.
A;M. J. Hum. Genet. 56, 716-724, 1995
A;Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sach A;Reference number: 151882; MUID:95193801; PMID:7887427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain DJ region (clone Cl13-105) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1327
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
B;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A;Title: Predominance of fetal type DJH joining in young children with B precursor lympi
A;Reference number: PH1302
A;Accession: PH1327
A;Molecule type: DNA
A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin
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R;Fetzner, S.; Muller, R.; Lingens, F.
Bacteriol. 14, 279-290, 1995
A;Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-comp. A;Reference number: A44920; MUID:92104974; PMID:1370284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-halobenzoate 1,2-dioxygenase component A beta chain - Pseudomonas cepacia (fragment)
C;Species: Pseudomonas cepacia
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                                                                                    C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: 164829
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross_references: GB:S76984; NID:g912781; PIDN:AAD14243.1; PID:g4261943
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Pred. No. 9.6e+02;
0; Mismatches 1.
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase
                                                                                     gene HEXA protein - human (fragment)
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A,Modecule type: protein
A,Residues: 1.14 <FBT>
A,Cross-references: UNIPROT:Q9RSQ6
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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8 SILW 11
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proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C;Species: Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Species: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C;Accession: S69123
R;Diggle, C; Hutton, M; Jones, G.R; Thomas, C.M.; Jackson, J.B.
R;Diggle, C; Hutton, M; Jones, G.R; Thomas, C.M.; Jackson, J.B.
A;Title: Properties of the soluble polypeptide of the proton-translocating transhydrogen
A;Reference number: S69123; MUID:95255277; PMID:7737169
A;Accession: S69123
A;
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Arch. Blochem. Blophys. 316, 572-584, 1995
A;Title: Methionine blosynthesis in higher plants. I. Purification and characterization
A;Reference number: 869159; MUID:95142682; PMID:7840669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Exp. Med. 174, 115-124, 1991
A;Title: Unnctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0586
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A;Molecule type: mRNA
A;Residues: 1-7 <FEB.
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor
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C.Species: Mus musculus (house mouse)
C.Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Accession: PTG586; PTG592
G.Beney, A.J.
J. Exp. Med 174 115
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C;Species: Spinacia oleracea (spinach)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 2; Length 12;
Pred. No. 5.2e+02;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.2%;
Matches 2; Conservative
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Best Local Similarity 50.0°
Matches 4; Conservative
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Matches 4; Conservative
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R; Ravanel, S.; Drow
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 14, 2004, 13:32:33 ; Search time 22.5 Seconds (without alignments) 59.868 Million cell updates/sec Run on:

US-09-831-253F-6

71 1 TSLDASIIWAMMON 14 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

2096 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 14

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\* Database

piri: piri: piri:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote		proton-translocati	T-cell receptor be	cystathionine gamm	gene HEXA protein	Ig heavy chain DJ	2-halobenzoate 1,2	T cell receptor al	T-cell receptor be	hypothetical prote	Iq H chain V-D-J r	processing enzyme,	T cell receptor al	alcohol dehydrogen	phosphoenolpyruvat	polygalacturonase	alcohol dehydrogen	tyrosine 3-monooxy	aeg-46.5 protein -	T cell receptor al	T cell receptor al	ran	litorin - Rohde's					
	ΙD	A35105	PQ0731	869123	PT0586	869159	I64829	PH1327	A44920	PH1769	PT0519	809652	PH1602	S66248	PH1768	S66195	S13889	D61440	S66196	PN0581	PN0580	PN0579	PN0577	PN0576	PN0578	I54984	PH1758	PH1766	S14336	S07241
	DB	2	~	7	~	~	~	~	~	7	0	0	~	~	~	~	~	~	~	N	C3	~	N	0	N	~	N	~	N	~
	Length	14	7	12		10	12	14	14	14	9	7	7	10	14	9	a	10	11	12	12	12	12	12	12	13	14	14	14	თ
	당성	6.6	0.1	0.1	9.6	9.6	9.6	9.6	9.6	3.2	5.8	8.8	9.	6.8	9.8	4.0	4.0	5.4	25.4	5.4	4.	5.4	4.0	5.4	4.0	5.4	5.4	4.	4.	œ.
de	Mat	36	e	Ä	ñ	ñ	2,	5	5	8	56	26	56	26	56	2	2	25	23	2	2	23	2,	23	25	25	25	23	2	2
	Score	26	22	22	21	21	21	21	21	20	19	19	19	19	19	18	18	18	18	18	18	18	18	18	18	18	18	18	18	17
	Result No.	-	7	Э	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	56		28	29

gene c-mpl protein	bacterioferritin -	hypothetical prote	pneumadin - human	pneumadin - rat	phospholipase A2 (	T cell receptor V-	T cell receptor al	T cell receptor al	T cell receptor al	glucuronosyltransf	glycine reductase	litorin 2-Glu - Au	litorin I - Austra	neuromedin C - bov	neuromedin C - lau	
I58350	S48182	A35556	B33143	A33143	A29169	S57567	PH1757	PH1759	PH1767	PX0008	A39308	S07205	S07204	A60647	PQ0177	
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Ø	10	10	10	10	12	13	14	14	14	7	80	σ	σ	10	10	
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23.	33	23.	23.	23	23.	23.	23.	23.	23.	22.	22.	22.	22.	22.	22.	
17				17												
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: mitochondrion Neurospora crassa
C;Species: mitochondrion Neurospora crassa
C;Species: mitochondrion Neurospora crassa
C;Species: mitochondrion
A35105
R;Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora
A;Reference number: A35105, MUID:90263093; PMID:2160856
A;Accession: A35105
A;Accession: A35105
A;Accession: A35105
A;Accession: A35105
A;Accession: A35105
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
C;Keywords: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion
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Pred. No. 1.1e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.5%;
Matches 3; Conservative
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6 SIIWAMMQ 13 | :| ::| 2 SFLWTLLQ 9 q ઠ

PQ0731
unidentified 5.7/35K protein [imported] - rice (fragment)
unidentified 5.7/35K protein [imported] - rice (fragment)
unidentified 5.7/35K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence\_revision 1
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
Theor. Appl. Genet. 86, 935-942, 1993
A;Reference number: PQ0696
A;Reference number: PQ0696

A;Status: preliminary A;Molecule type: protein A;Residues: 1-11 <KOM A;Cross-references: UNIPROT:Q7M1U2

Gaps ö h Similarity 40.0%; Pred. No. 4.7e+02; 2; Conservative 3; Mismatches 0; Indels Query Match Best Local Similarity Matches 2; Conserv

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Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,141A
FILING DATE: 06-UM-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY CHRISTINE B.
REFERENCE/DOCKET NUMBER: 1746IIB
FELEPANTION NUMBER: 1761IB
FELEPANTION NOW: (909) -594-6734
TELEPANTION FOR SEQ ID-NO: 32:
FELEPANTION FOR SEQ ID-NO: 32:
ENGURNCE CHRRACTERISTICS:
LENGTH: 15 amino acids
TYPE: Amino
```

Search completed: November 14, 2004, 12:08:49 Job time : 12.0213 secs

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4 DASIIWA 10

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REFERENCE/DOCKET NUMBER: 0233 US

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Sequence 15, Application PC/TUS9500062
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc.
IIILE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESSONDENCE ADDRESS:
ADDRESSE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
                                                                                                                                                                                                                                                   STATE: lowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/Microsoft Windows
SOFTWARE: Microsoft Windows Notepad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.4
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-00062-15
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Patent No. 5717061

GENERAL INFORMATION:
APPLICANT: Rao, Gururaj A.
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: STREET: 7100 N.W. 62nd Avenue
CITY: Johnston.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 1; Lengtn 23, Pred. No. 2.5e+02;
                                                                                                                                                                                                                                              Score 28; DB 1; Length 23;
Pred. No. 2.5e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,174A
FILING DATE: 12-MAY-1995
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,512
FILING DATE: 18-UN-1993
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bobrowicz, Donna
REGISTRATION NUMBER: 32,196
REFERENCE/DOCKET NUMBER: 0234R2D-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 245-3594
TELEFAX: (515) 245-3634
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (515) 248-4896
TELEFAX: (515) 334-6883
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                   39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 23 amino TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IIWAMM 12
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Gaps
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APPLICANT: MUMPORD, RICHARD A.
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: BOGER, JOSHUA S.
TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE B. CARTY
STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 5; Length 23;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Yates, Michael E.; Sweeney, Patricia A.;
NAME: Roth, Michael J.; & Simon, Soma G.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 448-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
12-08-469-141A-32
5 Sequence 32, Application US/08469141A
Patent No. 6124107
                                                                                                                                                                                                                                                                               TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: RAHWAY
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM Compatible FORM:
OPERATING SYSTEM: MS-DOS/Microsoft Windows SOFTWARE: Microsoft Windows No. 5607914epad CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,632
FILING DATE: 07-JAN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/079,512
APPLICATION NUMBER: 08/18/93
ATTORNEY/AGENT INFORMATION:
NAME: ROGIL Michael J.
REGISTRATION NUMBER: 29,342
                             Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Seguence
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1 LOADVLWOM 9
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5 NMLWNMMQ 12
US-08-485-508-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 108
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                               39.4%; Score 28; DB 1; Length 12; 66.7%; Pred. No. 1.3e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFFWALING SISLEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION S 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: US 07/081,395
FILING DATE: 06-MAY-1992
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000324-002/1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REPERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ 1D NO: 50: SEQUENCE CHARACTERISTICS: TENGTH: 12 amino acids
                  12 amino acids
                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 4; Conservative
 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                             , MOLECULE TYPE: peptide US-08-485-508-34
                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                8 IWAMMQ 13
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US-08-485-508-50
                  LENGTH:
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                                                                                                                                                                                                                                                                                  "Sequence 108, Application US/09255501
| Sequence 108, Application US/09255501
| Patent No. 6596525
| GENERAL INFORMATION:
| APPLICANT: Betell, David
| APPLICANT: Betell, David
| TITLE OF INVENTION: HUMANY PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN TITLE OF INVENTION: HUMANY AND METHODS FOR CONSTRUCTING, IDENTIFYING AND FILE REFERENCE: GCS27
| CURRENT APPLICANTION: PRODUCING SUCH PROTEINS
| FILE REFERENCE: GCS27
| CURRENT PELICATION NUMBER: US/09/255,501
| CURRENT PILING DATE: 1999-02-23
| NUMBER OF SEQ ID NOS: 211
| SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-255-501-108
                                                                ;
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Sequence 15, Application US/08179632

Patent No. 5607914

GENERAL INFORMATION:
APPLICANT: Rao, A. Gururaj; Zhong, Lingxiu
ATITLE OF INVENTION: SYRTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
COUNTRY: United States
COUNTRY: United States
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.4%; Score 28; DB 4; Length 15; Best Local Similarity 44.4%; Pred. No. 1.6e+02; Matches 4; Conservative 2; Mismatches 3; Indels
                                                             1; Indels
Score 28; DB 1; I
Pred. No. 1.3e+02;
3; Mismatches 1;
```

```
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 1; Length 12; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALLE: 94304
CAPPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NOWER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 16-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
                       000324-046/1056.1
                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000324-002/1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Affymax Technologies, NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08485508 Patent No. 5786322
                    REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
  36,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cwirla, Steven E. Dower, William J. Koller, Kerry J.
                                                                                                                                                                                                                                                                                                                                                   39.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 4001 Miranda Ave.
Palo Alto
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                        LENGTH: 12 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::| |||
5 NMLWNMMQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 SIIWAMMO 13
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                  TYPE: amino & STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DO APPLICANT: KC APPLICANT: LA APPLICANT: LA APPLICANT: MA APPLICANT: RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94304
                                                                                                                                                                                                                                                                                                  US-08-439-817-30
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APPLICANT: Cwirla, Steven E.

APPLICANT: Dower, William J.

APPLICANT: Dower, William J.

APPLICANT: Lee, Jung

APPLICANT: Martens, Christine L.

APPLICANT: Ruhland-Fritsch, Beatrice

TITLE OF INVENTION: Peptides and Compounds That Bind

TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion

TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion

TITLE OF INVENTION: Molecule I (ELAM-1)

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSE: Afframa Technologies, NV

STREET: A001 Miranda Ave.

CITY: Palo Alto

STREET: A01 Miranda Ave.

CONTEX: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.4%; Score 28; DB 1; Length 12; 66.7%; Pred. No. 1.3e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTHE: IBM PC compatible
CORFWARE: PatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/21,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/21,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING NUMBER: US 07/881,395
ATTENT NUMBER: US 07/881,395
ATTENT NUMBER: US 07/881,395
                    FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: SEEVENE, LAUREN L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 36,691
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFRAX: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
JMBER: US 08/057,295
05-MAY-1993
                                                                                                                                                                                                                                                                     TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stevens, Lauren L
                                                                                                                                                                                                                                                                                                                                                   12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 IWAMMQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LWVMMO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-439-817-14
                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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APPLICANT: Barrett, Ronald W.
APPLICANT: Barrett, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Koller, Kerry J.
APPLICANT: Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Barrens, Christine L.
APPLICANT: Christine L.
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 1; Length 12;
Pred. No. 1.3e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-LUOS/MS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
FILING DATE: 16-FEB-1996
FILING DATE: 0-MAY-1993
FILING DATE: 0-MAY-1993
FRICK APPLICATION NUMBER: US 07/881,395
FILING DATE: 0-MAY-1993
FRICK APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1993
FREFERENCE/DOCKET NUMBER: 1023.1A
FREFERENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 14, Application US/08439817; Patent No. 5728802
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4001 Miranda Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SIIWAMMO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S NMLWNWMO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-390-156A-22
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0
darrett, Ronald W.

APPLICANT: Dower, William J.
TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: Affymax Technologies, N.V.
STREET: California
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08390156A

Sequence 22, Application US/08390156A

Patent No. 5648458

GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: BLAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 1; Length 12;
Pred. No. 1.38+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: OF-MS-1996
PRING APPLICATION DAMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATFORNEY/AGENT INFORMATION:
NAME: SAWISS, Gerald F.
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REJERMA: 415-496-2300
TELEPHONE: 415-496-2300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.77
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bingle
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STRANDEDNESS: Bir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 IWAMMO 13
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7 LWVMMQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-241-054-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritisch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
                                                                                                                                                       Gaps
; ORGANISM: Artificial Sequence
; FEATURE:
; CTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.4%; Score 28; DB 1; Length·12; 66.7%; Pred. No. 1.38+02; tive 1; Mismatches 1; Indels
                                                                                                        40.8%; Score 29; DB 4; Length 15; 40.0%; Pred. No. 1.1e+02; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 530
ADD: APPLICATION -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia COUNTKY: USA ZIP: 22313
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 3.5.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTATION NUMBER: 30,113
REGISTATION NUMBER: 30,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 000324-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08241054
Patent No. 5643873
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Barrett, Ronald W. Cwirla, Steven E. Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.73
Matches 4; Conservative
                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                                                                       3 TLQADVLWQM 12
                                                                                                                                                                                            2 SLDASIIWAM 11
                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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APPLICANT: Martens, Christine L.
APPLICANT: Rahland-Fritsch, Beatrice
APPLICANT: Rahland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.4%; Score 28; DB 1; Length 12; 50.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/21,054
FILING DATE: 11-MAY-1994
CLASSIPRICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-WAY-1993
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-WAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: GGEAD F. SWISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-390-156A-14
Sequence 14, Application US/08390156A
Patent No. 5648458
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
Sequence 50, Application US/08241054
Patent No. 5643873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,113
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TELEPHONE: 415-854-7400
                                                                   Barrett, Ronald W. Cwirla, Steven E. Dower, William J.
                                                                                                                                              Koller, Kerry J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                         Lee, Jung
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Matches 4; Conserv
                                                GENERAL INFORMATION:
APPLICANT: Barret
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US-09-255-501-106
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LENGTH: 15
TYPE: PRT
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LENGTH: 15
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15, Appl
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Sequence 107, App
Sequence 34, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 30, Appl
Sequence 34, Appl
Sequence 36, Appl
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Sequence 4, Appli
Sequence 5, Appli
Sequence 149, App
Sequence 110, App
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                                                                                                                    ; Search time 11.0213 Seconds (without alignments) 84.242 Million cell updates/sec
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Sequence 4
Sequence 3
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Sequence 3
Sequence 5
Sequence 1
Sequence 1
Sequence 2
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Sequence 3
Sequence 3
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-241-054-50
US-08-241-054-50
US-08-390-156A-14
US-08-390-156A-22
US-08-439-817-30
US-08-439-817-30
US-08-439-817-30
US-08-439-817-30
US-08-439-817-30
US-08-485-508-50
US-08-485-508-34
US-08-140-174A-15
PCT-US95-00062-38
US-08-440-174A-15
US-08-440-174A-15
US-08-440-174A-15
US-08-64-948-39
US-09-073-010-38
US-09-073-010-38
US-09-064-839-4
US-08-24-839-4
US-08-24-839-4
US-08-24-945-39
US-08-24-945-39
US-08-24-945-39
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US-09-428-082B-149
US-08-241-054-110
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                                                                                                                                                                                                                                                                                                                      478139 segs, 66318000 residues
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                                                                                                                        November 14, 2004, 11:57:26
                                                                                   OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 23
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Maximum DB seq
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                                                             Sequence 106, Application US/0925501
Patent No. 659525
GENERAL INFORMATION:
APPLICANT: Estell, David
APPLICANT: Harding, Fiona
TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
TITLE OF INVENTION: PRODUCING SUCH PROTEINS
FILE REFERENCE: GC527
CURRENT APPLICATION NUMBER: US/09/255,501
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 211
SOUTTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107, Application US/09255501

Patent No. 6596525
GENERAL INFORMATION:
APPLICANT: Estell, David
TITLE OF INVENTION: HUMANY PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
TITLE OF INVENTION: HUMANY AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
TITLE OF INVENTION: HOWEVER SUCH PROTEINS
FILE REFERENCE: GC527
CURRENT APPLICATION NUMBER: US/09/255,501
CURRENT PILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 211
SOUTHWARE: PATENTIN Ver. 2.1
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         US-08-439-817-90
US-08-439-817-90
US-09-082-508-110
US-08-64-496-2
US-08-630-052-13
US-08-630-052-13
PCT-US92-09307-13
US-08-388-772-27
US-08-586-772-27
US-08-586-772-27
US-09-559-512-27
US-09-053-611-29
US-09-053-611-29
US-09-053-611-29
US-09-053-611-29
US-09-053-611-29
US-09-053-611-29
US-09-053-611-29
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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6 TLQADVLWQM 15
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APPLICANT: KIRST, Susan J.
APPLICANT: KIRST, Susan J.
APPLICANT: HOLTZMAN, Douglas A.
APPLICANT: FRASER, Christopher C.
APPLICANT: SHARP, John D.
APPLICANT: SHARP, John D.
APPLICANT: SHARP, John D.
APPLICANT: BARNES, Thomas S.
TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER FILER REFERENCE: 10147-1103
CURRENT APPLICATION NUMBER: US 09/596,194
PRIOR PILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-66-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.4%; Score 28; DB 14; Length 20; 50.0%; Pred. No. 6.6e+02; tive 2; Mismatches 3; Indels
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
; LEWGTH: 20
; LEWE: PRT:
; ORGANISM: HOMO-sapiens
US-09-759-1308-296
                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-189-123-26
Sequence 26, Application US/10189123
Publication No. US20030082586A1
GENERAL INFORMATION:
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Best Local Similarity 50.0
Matches 5; Conservative
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| SLRTVVIWAL 14
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; ORGANISM: Homo sapiens
US-10-189-123-26
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Gaps
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                                APPLICANT: Thompson, Scott A
APPLICANT: Thompson, Scott A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR PILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin version 3.2
SEQ ID NO 1234
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 15; Length 22;
Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 296, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: GAGE-1 segment 9
US-10-296-734-1234
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US20040054137A1
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Myers, Paul S
Leiby, Kevin R
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Goodearl, Andrew
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Kirst, Susan J
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Best Local Similarity 50.v.
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ORGANISM: Artificial
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                                                                                                            APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REPERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 00/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PARENT IN version 3.1
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Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                           Sequence 1338, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
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COTHER INFORMATION: DGI-2-20R-4-E6
US-10-280-066-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
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ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-225-567A-1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ASIIWAMMQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARIIWSLRQ 9
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US-10-296-734-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1338
LENGTH: 20
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LENGTH: 20
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Query Match 40.8%; Score 29; DB 14; Length 17; Best Local Similarity 66.7%; Pred. No. 3.7e+02; Matches 6; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                    US-10-176-791A-76

Sequence 76, Application US/10176791A

Sequence 76, Application US/10176791A

Publication No. US20030237101A1

GENERAL INFEMATION:
APPLICANT: WEHRLE-HALLER, BERNHARD M.

APPLICANT: MHOF, BEAT A.

TITLE OF INVENTION: Basolateral Sorting Signal and TITLE OF INVENTION: Enabletors Thereof FILE REFERENCE: 50275/002001

CURRENT APPLICATION NUMBER: US/10/176,791A

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: PCT/CH99/00624

PRIOR PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 76

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 76

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Junction of Tac-Tyr Chimera
US-10-176-791A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-657-022-606
Sequence 606, Application US/10657022
Publication No. US20040180354A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
TITLE NF INVENTION: BETTOPE SEQUENCES
FILLE REFERENCE: MANIN. 032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: 60/409123
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 4; Conservative
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; ORGANISM: Homosapiens
US-10-657-022-606
                                     7 IIWAMMON 14
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40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                               Query Match
40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels
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40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 299, Application US/10657022; Publication No. US20040180354A1; GENERAL INFORMATION.

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

APPLICANT: Liu, Liping

APPLICANT: Liu, Liping

TTILE OF INVENTION: EPITOPE SEQUENCES

FILE REFERENCE: MANNK.032A

CURRENT APPLICATION NUMBER: US/10/657,022

CURRENT FILING DATE: 2003-09-04

PRIOR FILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 610

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 299
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Publication No. US20040180354A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNER: 03/10/657,022
CURRENT APPLICATION NUMBER: 05/409123
FRIOR PELING DATE: 2003-09-04
RIOR REDIT OF SEQ ID NOS: 610
SOFTWARE: PESESEC for Windows Version 4.0
SEQ ID NO 301
LENGTH: 10
TYPE: PRT
TYPE: PR
                                                          TYPE: PRT
ORGANISM: Homosapiens
US-10-657-022-294
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US-10-657-022-299
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2 ILWLLMNN 9
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                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
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50.0%; Pred. No. 1.4e+06;
iive 2; Mismatches 2,
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           TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNK.032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: 60/409123
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 295
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 294, Application US/10657022
Publication No. US20040180354A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Simand, John J. L.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-06
PRIOR FILING DATE: 2003-09-06
PRIOR FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Zheng
TITLE OF INVENTION: EPITOPE SEQUENCES
TITLE OF INVENTION: EPITOPE SEQUENCES
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FILING DATE: 2002-09-04
PRIOR PPLICATION NUMBER: 60/409123
PRIOR PLING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 610
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 300
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 300, Application US/10657022
Publication No. US20040180354A1
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Best Local Similarity 50...
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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US-10-657-022-300
                                                                                                                                                                                                                                                                   ORGANISM: Homosapiens
US-10-657-022-295
                                                                                                                                                                                                                                                                                                                                                                                                                                   7 IIWAMMON 14
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  Liu, Zheng
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 14; Length 22;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
              GENERAL INPORMATION:
APPLICANT: Rosen et. al
FITLE OF INVENTION: 101 Human Secreted Proteins
FITLE OF INVENTION: 101 Human Secreted Proteins
FILE REFERENCE: PSC17P1
CURRENT APPLICATION NUMBER: US/10/195,730
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 06/060,837
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,862
PRIOR APPLICATION NUMBER: 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 390
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 319
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION TO THE ADDITION: 101 Human Secreted Proteins FILE REFERENCE: PZ017P1
CURRENT APPLICATION NUMBER: US/10/799,747
CURRENT FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: US/09/281,976
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-10-02
PRIOR APPLICATION NUMBER: 60/060,862
PRIOR APPLICATION NUMBER: 60/060,862
PRIOR PILING DATE: 1997-10-02
PRIOR PILING DATE: 1997-10-02
PRIOR PILING DATE: 1997-10-02
PRIOR PILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 390
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4; Mismatches
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Publication No. US20040180354A1
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Publication No. US20040157258A1
GENERAL INFORMATION:
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Publication No. US20030144492A1
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GENERAL INPORMATION:
APPLICANT: Simaru, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0.
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TSLDASIIWA 10
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STLDRSVIWS 13
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-10-657-022-295
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LENGTH: 22
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; OTHER INFORMATION: Myostatin Binding Peptide
US-10-742-379-441
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US-10-195-730-319
; Sequence 319, Application US/10195730
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Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSLDASIIWAMMQ 13
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Sequence 319, App
Sequence 395, App
Sequence 300, App
Sequence 294, App
Sequence 299, App
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Sequence 76, Appl
Sequence 606, App
Sequence 1338, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 606, App
Sequence 1338, Ap
Sequence 90, Appl
Sequence 1234, Ap
                                                                                                            November 14, 2004, 12:03:21; Search time 33.0638 Seconds (without alignments) 149.815 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/PcT_NEW_PUB.Popp:*

2: /cgn2_6/ptodata/1/pubpaa/PcT_NEW_PUB.Popp:*

3: /cgn2_6/ptodata/1/pubpaa/RcT_NEW_PUB.Popp:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.Popp:*

5: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.Popp:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.Popp:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.Popp:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.Popp:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.Popp:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.Popp:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.Popp:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.Popp:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.Popp:*

14: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.Popp:*

15: /cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.Popp:*

16: /cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.Popp:*

17: /cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.Popp:*

18: /cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.Popp:*

19: /cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.Popp:*

10: /cgn2_6/ptodata/1/pubpaa/USO0PUBCOMB.Popp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-195-730-319
US-10-657-022-395
US-10-657-022-394
US-10-657-022-294
US-10-657-022-299
US-10-657-022-391
US-10-657-022-391
US-10-156-731-38
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                  1568699 seqs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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71
1 TSLDASIIWAMMQN 14
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Match Length
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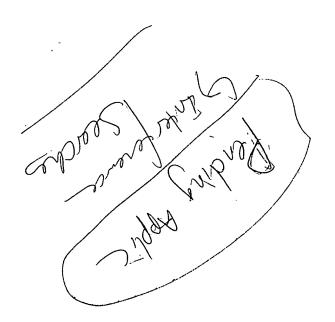
Gaps

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Score 36; DB 16; Length 22; Pred. No. 29; Mismatches 3; Indels

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Sequence 41, Appl Sequence 44, Appl Sequence 44, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 35, Appl Sequence 38, Appl Sequence 28, Appl Sequence 25, Appl Sequence 25,
                                               Seguence 26, Appl
Seguence 296, App
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Sequence 149, App
Sequence 149, App
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Sequence 13, Appl
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Sequence 77,
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; Sequence 441, Application US/10742379
; Bublication No. US20040181033A1
; GENERAL INFORMATION:
    APPLICANT: Han, HO
; APPLICANT: Han, HO
; APPLICANT: Boone, Thomas Charles
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN
; FILE REPREBLICATION NUMBER: US/10/742,379
; CURRENT FILING DATE: 2003-12-19
; PRIOR PILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 634
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 41
; LENGTH: 22
US-10-609-217-149
US-10-632-388-149
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TISSUE-Blood;

MEDLINE-96121606; PubMed=8595431;

MEDLINE-96121606; PubMed=8595431;

MEDLINE-96121606; PubMed=8595431;

MEDLINE-96121606; PubMed=8595431;

Tovel missense mutation of Asp328 to Val in Linker 12 domain of Keratin 5.";

Hum. Mol. Genet. 4:1999-2000(1995).

E MBML. D50666; BAA09320.1; -.

R GO: C0:0005882; C:intermediate filament; IEA.

Keratin.

T NON_TER 1 1

T NON_TER 23 23

NON_TER 23 23

SEQÜENCE 23 AA; 2546 MW; 6BA5FFB4FC7E511E CRC64;
                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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32.4%; Score 23; DB 2; Length 23;
Best Local Similarity 36.4%; Pred. No. 5.3e+03;
Matches 4; Conservative 3; Mismatches 4; Indels
Query Match 32.4%; Score 23; DB 2; Length 23; Best Local Similarity 25.0%; Pred. No. 5.3e+03; Matches 3; Conservative 5; Mismatches 4; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Keratin (Fragment)
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12 TIINRRLFWAII 23
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Q9UEK9;
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AC 090EK
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DT 01-MA
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Search completed: November 14, 2004, 12:07:34 Job time : 38.383 secs

4 DASIIWAMMON 14 | |:::| | DISVVLSMDNN 15

8 8

Created) Last sequence update) Last annotation update)

24, 24, 25,

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MEDLINE=92352338; PubMed=1339264;
Mendez E., Arias C.F., Lopez S.;
"Genomic rearrangements in human rotavirus strain Wa; analysis of
                                                                                                                                                                                                                                                                                                                               EMBL; S41238; AAP13880.1; -.
GG; GG:0003723; F:RNA binding; IEA.
InterPro; IPR002873; Rota NGP3.
SEQUENCE 22 AA; 2242 MW; 22CC217A1F6BD3AA CRC64;
                                                                                                                                                          Human rotavirus A.
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                         Arch. Virol. 125:331-338(1992).
EMBL; S41238; AAP13880.1; -.
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Best Local Similarity 40...
Best A; Conservative
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                                                      PRELIMINARY;
                                                                                01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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8 TSFEAAVVAA 17
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                                                                                                                                                                                    NCBI_TaxID=10941;
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                                                                                                                                             Name=gene 7;
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                                                                    Q80GP4;
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                                                                                                                               Gene 7
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Q7S8F9
                        RESULT 13
Q80GP4
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Ward L.J., Beresford T.P., Lubbers M.W., Jarvis B.D., Jarvis A.W.;
"Sequence analysis of the lysin gene region of the prolate lactococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequencing and analysis of the prolate-headed lactococcal bacteriophage c2 genome and identification of the structural genes."; Appl. Environ. Microbiol. 61:4348-4356(1995).

SEMBL, 148605; AAA92170.1; SEQUENCE 22 AA; 2631 MW; 1DFFIFA427364C93 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2001 (TrEMBLrel. 16, Last annotation update)
CUSATIVIN (Fragment).
Cucumis sativus (Cucumber).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; eurosids 1; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95115663; PubMed-7816023;
Lubbers M.W., Ward L.J., Beresford T.P., Jarvis B.D., Jarvis A.W.;
"Sequencing and analysis of the cos region of the lactococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses, dsDNA viruses, no RNA stage, Caudovirales; Siphoviridae,
c2-like viruses.
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Rojo M.A., Arias F.J., Iglesias R., Ferreras J.M., Munoz R.,
Escarmis C., Soriano F., Lopez-Fando J., Mendez E., Girbes T.;
Planta 194:328-338(1994).
SEQUENCE 21 AA; 2347 MW; FCD26FB44DB60ACC CRC64;
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MEDLINE=96086019; PubMed=8534101;
Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W.,
                                                                                                                                                                                                                                                                          32.4%; Score 23; DB 2; Length 21; 33.3%; Pred. No. 4.8e+03; Live 3; Mismatches 1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             22 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteriophage c2.";
Mol. Gen. Genet. 245:160-166(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus bacteriophage c2
                                                                                                                                                                                                                                                                           Query Match 32.4
Best Local Similarity 33.3
Matches 2; Conservative
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7 DLNVVW 12
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Gaps

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Score 23; DB 2; Length 22; Pred. No. 5e+03; 4; Mismatches 2; Indele

32.4%;

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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
A Gui D., Ianakiev P., Pedersen D., Nielson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kothe G.C., Jedd G., Mawes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Greenberg D.,
A Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
A Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
T.The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, AABX01000232; EAA32642.1; -. SEQUENCE 23 AA; 2598 MW; 7EA10217A542BCC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                         Created)
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PRELIMINARY;
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6 TSYDLFINW--MKN 17

Matches

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SEQUENCE FROM N.A.

MEDLINE=87089706; PubMed=3025606;

MEDLINE=87089706; PubMed=3025606;

"Transcriptional control signals of a herpes simplex virus type 1 late (gamma-2) gene lie within bases -34 to +124 relative to the 5' terminus of the mRNA.";

Mol. Cell. Biol. 6:3652-3666(1986).

EMBL; M14128; AAA45784.1; -.

NON TER. 17 17 17
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Biochemistry 27:678-686(1988).
PIR; A28702; A28702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
MEDLINE-88163652; PubMed=3349056;
Sugita O., Sassa S., Miyairi S., Fishman J., Kubota I., Noguchi T.,
Kappas A.;
                                                                                                                                                                                HSV-1 glycoprotein C (Fragment).

Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).

Viruses; dabNa viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 2; Length 17;
Pred. No. 3.8e+03;
5; Mismatches 1; Indels
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                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome P450-C-M/F, hepatic (Fragment).
Rattus norvegicus (Rat)
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Pred. No. 4.3e+03;
2; Mismatches 0;
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25.0%;
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9 AVVLWSLL 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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Q9S8L0
ID Q9S8L0
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Q7M0C6
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                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.; "Molecular and physiological responses to abscisic acid and salts in roots of salt-sensitive and salt-tolerant Indica rice varieties."; Plant Physiol. 107:177-186(1995).
Gramene; Q9S818; -. SEQUENCE 18 AA; 2097 MW; 146450D9A97E6D83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                VAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
40 kDa PI 8.5 ABSCISSIC acid-induced protein (Fragment).
07vza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrarcideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome oxidase II (Fragment).
Xylocopa virginica (Carpenter bee).
Mitochondrion.
   Pred. No. 1.7e+03;
2; Mismatches 1;
                                                                                                                                                                                      18 AA.
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EMBL, AF082918; AAD17778.1; --
GO, GO:0005739; C:mitochondrion; IBA.
                                                                                                                                                                                      PRT;
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MEDLINE=99152621; PubMed=10028295;
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95175599; PubMed=7870812;
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18 AA; 2202 MW;
50.08;
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Best Local Similarity 50.0.
7; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
 Similarity 50.0
3; Conservative
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DESVLW 15
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                                                       DASIIW 9
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NCBI_TaxID=28638;
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SEQUENCE
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MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
Kelley J.M., Cotton M.D., weidman J.F., Fujii C., Bowman C.,
Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
Smith H.O., Praser C.M., Vonter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the gastric pathogen Helicobacter
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
40 kDa PI 8.5 ABSCISSIC acid-induced histidine rich protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; DB 2; Length 22; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pylori.";
Nature 388:539-547(1997).
EMBL; AE000542; AAD07297.1; -.
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                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                Hypothetical protein HP0225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=HP0225;
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                                                                                                                                                                        PRELIMINARY;
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1 MDESYIWPIV 10
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|9 VLWVILKN 16
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SEQUENCE FROM N.A.
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025012
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NCBI_TaxID=5665;
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SEQUENCE 20 AA; 2203 MW; FEIA260FAIDBE41F CRC64;
                                                                                                                                       Score 27; DB 2; Length 19;
Pred. No. 7.4e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 2; Length 20;
Pred. No. 7.8e+02;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
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EMBL, AE009334; AAL64964.1; -1.
Complete protecome; Hypothetical protein.
SEQUENCE 18 AA; 2262 MW; BCFF4D6923A98943 CRC64;
                                                                                  B964CCC7FDAC36C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Cathepsin B-like cysteine protease (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PAE3501a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA.
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  GO; GO:0005739; C:mitochondrion; IEA
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MEDLINE=21664397; PubMed=11792869;
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                                                                                                                                       38.0%;
                                                        1 1
19 AA; 2291 MW;
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TSLNSFFNWLKMFN 19
                                                                                                                                                                                                                                                        1 TSLDASIIWAMMON 14
                                                                                                                                 Query Match
Best Local Similarity 42.9 Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity
Matches 4; Conserv
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                             Mitochondrion.
NON TER 19 ASEQÜENCE 19 A
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RESULT 4

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O6yid4 theromyzon
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monanthes i
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Baa00902 homo sapi
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
5- muclectide-forming nuclease (Fragment).
Lentinula edodes (Shitake mushroom) (Lentinus edodes).
Bukaryota; Fungi, Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Lentinula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kobayashi H., Inokuchi N., Koyama T., Tomita M., Irie M.; "Purification and characterization of the 2nd 5'-nucleotide-forming nuclease from Lentinus edodes.";
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Pubmed=10028295;
Dowton M., Austin A.D.;
"Evolutionary dynamics of a mitochondrial rearrangement 'hot spot'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
Braconidae; Doryctinae; Jarra.
NCBI_TaxID=64830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                       Q7m1j3
O77895
Q9r5q6
Q8s136
Q9twc0
Q9axw2
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Pred. No. 5.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008947; PLC Nuclease.
SEQUENCE 23 AA; 2535 WW; 978082B3B161FCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Cytochrome oxidase II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosci. Biotechnol. Biochem. 59:1169-1171(1995)
PIR; PC4030; PC4030.
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Q7MIJ3
                Q9PRQ1
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09R5Q6
08SL36
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Mol. Biol. Evol. 16:298-309(1999)
EMBL; AF034596; AAC79744.1; -.
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Les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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 ALDPSFVW 23
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Mitochondrion.
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Matches
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0964W7 leishmania
082802 pyrobaculum
025012 helicobacte
09881 oryza sativ
09503 xylocopa vi
069074 human herpe
07m0c6 rattus norv
098810 cucumis sativ
08084 nacrococcus
08084 homan rotav
07886 neurospora
08086 homo sapien
08048 human rotav
07988 neucospora
00798 neochromis
07789 orecohromis
07789 orecohromis
07789 archiophyto
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08016 trichophyto
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08016 trichophyto
08016 archioderma
061899 homo sapien
061899 homo sapien
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Q8w128 scaevola pr
Q9qv70 rattus sp.
Q49132 methylobact
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                                                                                                                 November 14, 2004, 11:57:26; Search time 37.383 Seconds (without alignments) 215.479 Million cell updates/sec
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                                  Compugen Ltd.
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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                                                                                                                                                                                                                                                                                                                 1825181 segs, 575374646 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Q6LAP9
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Q8W128
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Q8ZSZ9
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 23
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq
Maximum DB seq
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RESULT 10

US-08-390-156A-76

Sequence 76, Application US/08390156A

Patent No. 564848

GENERAL INFORMATION:
APPLICANT: Gwilla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: ELAM-1

TITLE OF INVENTION: ELAM-1
                                  36.6%; Score 26; DB 1; Length 12; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFFWALLY SYSTEM: PC-DOS/MS-DOS COFFWALLS FOR SYSTEM: PC-DOS/MS-DOS CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A FILING DATE: 16-FBE-1996
PRIOR APPLICATION NUMBER: US 08/057,295
PRIOR APPLICATION NUMBER: US 08/057,295
PRIOR APPLICATION NUMBER: US 07/881,395
PRIOR APPLICATION NUMBER: US 07/881,395
ATTORNEY/AGBNT INPORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/OFFCT NUMBER: 30,113
RELEPRANT A15-496-2300
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Pred. No. 2.7e+02;
                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-439-817-4
; Sequence 4, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.6%;
66.7%;
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Best Local Similarity 66.7
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                           Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: California
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APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Deven E.
APPLICANT: Deven E.
APPLICANT: Roller, Kerry J.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch, Beatrice
APPLICANT: Ruhland-Frisch
APPLICANT: Ruhland-
                                                                                                                                                                                                                                                                                                                                                             39.4%; Score 28; DB 1; Length 12; 50.0%; Pred. No. 1.3e+02; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSENCE BURNE, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STREET: 699 Prince Street
CITY: Alexandria
STATE: Uviginia
COUNTRY: USA
Z19: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-WAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-WAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-WAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-WAY-1993
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08241054
Patent No. 5643873
                    TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide US-08-241-054-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::| |||
5 NMLWNMMQ 12
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Gaps

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Length 12;

us-09-831-253f-6.closed.rai

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Selecting Including Endothelial Leukocyte Adhesion Molecule I
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US-09-428-082B-149

US-09-428-082B-149

US-09-428-082B-149

US-09-428-082B

Patent No. 6660843

Patent No. 6660843

Patent No. 6660843

PAPLICANT: FEIGE, ULRICH

APPLICANT: BOONE, THOMAS CHARLES

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527

CURRENT PEPLING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: 60/105,371

PRIOR APPLICATION NUMBER: 60/105,371

PRIOR PELING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133

SEQ ID NO 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                     Score 26; DB 1; I
Pred. No. 2.7e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000324-002/1056
                                                                                                 Affymax Technologies, NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stevens, Lauren L. REGISTRATION NUMBER: 36,691 REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                 4001 Miranda Ave
                                                           162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TITLE OF INVENTION: Pept
TITLE OF INVENTION: Sele
TITLE OF INVENTION: MOLE
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                     CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 IWAMMO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-485-508-5
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                                                     APPLICANT: KOLIET, KETY J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
TILE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304
ZIP: 94304
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PACHTION DATA:
APPLICATION NUMBER: US 08/04/19,817
FILING DATE: 11-MAY-1995
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTONEY/AGENT INPORMATION:
NAME: STEVENE LAUREN LAUREN LAUREN
NAME: ASEVERE LAUREN LAUREN
NAME: ASEVERE LAUREN LAUREN
NAME: ASEVERE LAUREN
TELEPRAK: 415-436-2300
INFORMATION FOR THE NO: 4:
SEQUENCE CHARACTERISTICS:
LEMERAL 12 AMINO GIGS

INFORMATION FOR SEQ ID NO: 4:
FELEPRATION OF 4:
SEQUENCE CHARACTERISTICS:
LEMERAL 12 AMINO GIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrett, Ronald W.
Cwirla, Steven E.
Dower, William J.
Koller, Kerry J.
Lee, Jung
Martens, Christine L.
Ruhland-Fritsch, Beatrice
                                                                                                                                                                                                                                  ADDRESSEE: Affymax Technologies, NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08485508
Patent No. 786322
GENERAL INFORMATION:
APPLICANT: CWITIA, Steven B.
APPLICANT: CWITIA, Steven B.
APPLICANT: CWITIA, Steven B.
APPLICANT: Lev, VILLIAM J.
APPLICANT: Lev, Unng
APPLICANT: Lev, Unng
APPLICANT: Reland-Fritsch, Beatri
 Barrett, Ronald w. Cwirla, Steven E. Dower, William J.
                                                                                                                                                                                                                                                STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.6
Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Sequence 29, Application US/09053611

Patent No. 6410245
GENERAL INFORMATION:
APPLICANT: NO. 6410245throp, Jeffrey P.
APPLICANT: Hart, Charles P.
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent
TITLE OF INVENTION: Nuclear Receptor and Coactivator Interactions
FILE REFERENCE: 2064
CURRENT APPLICATION NUMBER: US/09/053,611
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 40
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                                                                                                                                                                                                 0; Gaps
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; OTHER INFORMATION: Description of Artificial Sequence:Selected clone
US-09-053-611-29
                                                                                                                                            Query Match 36.6%; Score 26; DB 4; Length 12; Best Local Similarity 66.7%; Pred. No. 2.7e+02; Matches 4; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.2%; Score 25; DB 4; Length 12; Best Local Similarity 41.7%; Pred. No. 4e+02; Matches 5; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-842-164A-10
; Sequence 10, Application US/09842164A
; Patent No. 6544754
; GENERAL INFORMATION:
; APPLICANT: INOOTE, SATOSHI
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN
; FILE REFERENCE: 206497US0
; CURRENT APPLICATION NUMBER: US/09/842,164A
; CURRENT FILING DATE: 2001-04-26
; PRIOR FILING DATE: 2000-125053
                                             FEATURE:

COTHER INFORMATION: SELECTIN ANTAGONIST PEPTIDE
US-09-428-082B-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (11)...(11); OTHER INFORMATION: Xaa = any amino acid US-09-842-164A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Oplophorus gracilorostris
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SLDASIIWAMMQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                            8 IWAMMO 13
                                                                                                                                                                                                                                                                        : | | | | | | 7 LWDMMQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 29
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Ouery Match
Best Local Similarity 42.3%; Score 25; DB 4; Length 14;
Best Local Similarity 42.3%; Pred. No. 4.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 6 SIIWAWM 12
| :: | | :
| Db 5 SLLWKWL 11

Search completed: November 14, 2004, 13:46:47
Job time : 27.5 secs
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25; Search time 8.6383 Seconds

(without alignments)

155.938 Million cell updates/sec
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Title: US-09-831-253F-6
Perfect score: 71
Sequence: 1 TSLDASIIWANMQN 14
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0 Maximum DB seq length: 23 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

rRNA endonuclease hypothetical prote hypothetical prote T-cell receptor be cytochrome P450-C-Ig heavy chain bJ glutamate-ammonia unidentified 5.7/3 proton-translocati lactase-phlorizin hydroxypyruvate re cold-inducible pro killer toxin - year-cell receptor be cystathionine gamm gene HEXA protein Ig heavy chain DJ 2-halobenzoate 1,2 nikkómycin synthes protein C - oat (f kallikrein (PK-120 MHC class I transp trans-cinnamate 4-hemoglobin BIV - t L-lactate dehydrog dentinal fluid tra T cell receptory 7 alpha-hydroxy-4probable bacteriop Description SUMMARIES A64548 807966 807966 PH13262 PG0731 PG0731 PG0731 PG087 PG08 PC4030 A35105 DIRT PH1769 A45103 S61279 S29212 S50175 B59325 158038 S34739 S01816 Query Match Length DB Score Result No. 

SIIWAMMQ 13 | :| ::|

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T-cell receptor be	hypothetical prote	Ig H chain V-D-J r	processing enzyme,	T cell receptor al	T-cell receptor al	complement factor	transforming prote	probable trp opero	protein-tyrosine k	RNA-polymerase-ass	alcohol dehydrogen	phosphoenolpyruvat	polygalacturonase	alcohol dehydrogen	tyrosine 3-monooxy
PT0519	809652	PH1602	S66248	PH1768	PH0782	PL0109	A46236	AC0269	823361	A44139	866195	S13889	D61440	S66196	PN0581
~	~	7	0	~	~	N	~	~	N	~	N	7	7	~	7
9	7	7	10	14	15	15	16	20	21	21	9	σ	10	11	12
80	œ	œ	80	80	œ	80	80	œ	æ	80	4	4	4	4	4
26.	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.	25.4	25.4	25.4	25.	25.
19	19	19	19	19	19	19	19	19	19	19	18	18	18	18	18
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

PC4030
rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)
N'Allelnate names indicase her C'Species: Lentinula edodes (shiitake mushroom)
C;Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004 C;Accession: PC4030
R; Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.
biosci. biotecnhol. blochem. 59, 1169-11/1, 1995 A;Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease fr
A; Reference number: PC4030; MUID:95337563; PMID:7613009
A, Molecule type:
A;Residues: 1-23 <kob> A:Cross-references: UNIPROT:09UR71</kob>
C;Comment: This enzyme has 3'-nucleotidase activity. C;Keywords: endonuclease; hydrolase
Match 39.4%; Score 28;
best bocal Similarity 50.0%; Fred. NO. 81; Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SLDASIIW 9
Db 16 ALDPSFVW 23
RESULT 2
A15105 hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: mitochondrion Neurospora crassa C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text change 07-Dec-1999
C; Accession: A35105 R; Saville, B.f.; Collins, B.A.
Cell 61, 685-696, 1990
Ajilise: A Bite-Specific Beil-Cleavage reaction periormed by a novel KNA in heurospoid AjReference number: A35105; MUID:90263093; PMID:2160856
A:Accession: A35105 a.Status: preliminary: not compared with conceptual translation
A; Molecule type: DNA
A;Residues: 1-14 <sav> C;Genetics:</sav>
A;Genome: mitochondrion
A,Genetic code: SGC3 C,Keywords: mitochondrion
Similarity 37.5%, Pred. No. 1.1e+02
Si consettate si mismaccines si inters ci caps

Gaps

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A;Gene: CYP2D
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1326
R;Wasserman, R; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph A;Reference number: PH1302; MUID:93094761; PMID:1460419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T03261
R;Hirel, B.; Marsoller, M.C.; Hoarau, A.; Hoarau, J.; Brangeon, J.; Schafer, R.; Verma, Blant Mol. Biol. 20, 207-218, 1992
A;Title: Forcing expression of a soybean root glutamine synthetase gene in tobacco leave A;Reference number: Z14867; MUID:93004474; PMID:1356501
A;Accession: T03261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-23 <HTR>
A;Cross-references: UNIPROT:Q07939; EMBL:X68604; NID:g312275; PIDN:CAA48594.1; PID:g3122
C;Superfamily: glutamate-ammonia ligase
C;Keywords: cytosol; ligase
                                                                                     R;Sugita, O.; Sassa, S.; Miyairi, S.; Fishman, J.; Kubota, I.; Noguchi, T.; Kappas, A. Biochemistry 27, 678-686, 1988
A;Title: Cytochrome P-450-C-M/F, a new constitutive form of microsomal cytochrome P-450 A;Reference number: A28702; MUID:88163652; PMID:3349056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamate-ammonia ligase (EC 6.3.1.2), cytosolic - common tobacco (fragment) NiAlternate names: glutamine synthetesse (C.Species: Nicotiana tabacum (common tobacco) (C.Species: Nicotiana tabacum (common tobacco) (C.Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
| Species: Rattus norvegicus (Norway rat)
| Sate: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
| Accession: A28702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.4%; Score 23; DB 2; Length 19; 60.0%; Pred. No. 5.7e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain DJ region (clone C515-116) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 2; I
Pred. No. 7.1e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 2;
Pred. No. 6e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: PH1326
A,Molecule type: DNA
A,Residues: L-20 «WAS»
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                     A,Accession: A28702.
Molecule type: protein
A,Redides: 1-19 <SUG>
A,Cross-references: UNIPROT:Q7M0C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.4%;
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ilarity 50.0%;
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Best Local Similarity 50.v-
6, Conservative
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hes 3; Conserv
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown
Molecule type: DNA
A;Readuses: 1-22 <DNA
A;Cross-references: UNIPROT:O25012; GB:AE000542; GB:AE000511; NID:g2313310; PIDN:AAD0729
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A;Variety: strain C57BL/10
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C;Accession: S07966; S08057
C;Accession: S07966; S08057
C;Accession: Nogelee, J.; Appel, V.B.; White, J.; Horn, G.; Erlich, H.A.; Palmer, J. Exp. Med. 169, 115-133, 1989
A;Title: Molecular genetic analysis of 178 I-A(bm12)-reactive T cells.
A;Reference number: S05590; MUID:89080476; PMID:2783331
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                                                                                                                                   C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64548
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A;Reference number: S08057
A;Molecule type: mRNA
A;Residues: 1-19,21-22 <BIW>
A;Cross-references: EMBL:X14936; NID:g54884; PIDN:CAA33062.1; PID:g773251
C;Keywords: T-cell receptor
F;1-4/Domain: V region (W b-c--
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Pred. No. 1.8e+02;
5; Mismatches 1; Indels
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Best Local Similarity 25.0%;
Matches 2; Conservative
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9 VLWVILKN 16
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Matches 3; Conserv
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A;Molecule type: mRNA
A;Residues: 1-22 <BIL>
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Risuzuki, C.; Nikkuni, S.
Apric. Biol. Chem. 53, 2599-2604, 1989
Africle: Purification and properties of the killer toxin produced by a halotolerant yea
A;Reference number: PQ0007
A;Accession: PQ0007
A;Molecule type: protein
A;Residues: 1-22 <SUZ>
                                                                                                                                                                                                        hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)
C;Species: Methylobacterium extorquens
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A44921
R;Chistoserdova, L.V.; Lidstrom, M.E.
J. Bacteriol. 174, 71-77, 1992
A;Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase A;Reference number: A44921; MUID:92104992; PMID:1729225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cold-inducible protein, 70K - rainbow trout (fragment)

C;Species: Oncorbynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C;Accession: 562893

R;Yamashita, M.; Ojima, N.; Sakamoto, T.

R;Yamashita, M.; Ojima, N.; Sakamoto, T.

A;Title: Induction of proteins in response to cold acclimation of rainbow trout cells. A;Reference number: 562893; MuID:96184500; PMID:8605981

A;Accession: 562893

A;Accession: S62893

A;Accession: S62893

A;Estus: preliminary

A;Molecule type: protein

A;Residues: 1-21 < YAM>
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C,Species: Pichia farinosa
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
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66.7%; Pred. No. 9.3e+02;
iive 2; Mismatches 0;
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Best Local Similarity 66.7
Matches 4; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-20 <CHI>
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                                                                                                                                                 unidentified 5.7/35K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: PQ0731
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A;Reference number: PQ0696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C;Species: Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C;Accession: S69123
R;Diggle, C; Hutton, M; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Bur J. Biochem. 228, 719-726, 1995
A;Title: Properties of the soluble polypeptide of the proton-translocating transhydrogen
A;Reference number: S69123; MUID:95255277; PMID:7737169
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R;Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J. Biol. Chem. 2569, 13609-13616, 1993
A;Title: In vivo sucrase-isomaltase and lactase-phlorizin hydrolase turnover in the fed A;Reference number: A46592; WUID:93293888; PMID:8514793
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996
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40.0%; Pred. No. 4.7e+02;
iive 3; Mismatches 0; Indels
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A;Molecule type: protein
A;Residues: 1-19 cDUD:
A;Note: sequence extracted from NCBI backbone (NCBIP:134560)
C;Keywords: carbohydrate digestion; intestine
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Pred. No. 5.2e+02;
4; Mismatches 3;
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Modecule type: protein
A;Reddues: 1-11 <KOM>
A;Cross-references: UNIPROT:Q7MIU2
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22.2%;
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <DIG>
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Cystathionine gamma-synthase - spinach (fragment)
Cystathionine gamma-synthase - spinach)
C;Species: Spinacia oleracea (spinach)
C;Species: Spinacia oleracea (spinach)
C;Accession: S69159
R;Ravanel, S.; Droux, M.; Douce, R.
Artile: Methionine biosynthesis in higher plants. I. Purification and characterization A;Reference number: S69159; MUID:95142682; PMID:7840669
A;Accession: S69159
A;Accession: S69159
A;Accession: S69159
A;Accession: S69159
A;Accession: S69159
C;Reywords: Lio <ARV>
A;Cross-references: UNIPROT:Q7M1J3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
T;Feeney, A.J.
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUD:91277601; PMID:1711558
A;Recession: PT0586
A;Retus: translation not shown
A;Molecule type: mRNA
A;Retus: translation not shown
A;Molecule type: mRNA
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A;Retus: translation not shown
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A;Retus: translati
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A; Experimental source: strain KK1
A;Note: the full activity of this toxin depends on NaCl or KCl
                                                                                                                                                          Query Match 31.0%; Score 22; DB 2; Length 22; Best Local Similarity 37.5%; Pred. No. 1e+03; Matches 3; Conservative 3; Mismatches 2; Indels
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29.6%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels
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29.6%; Score 21; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.88+05;
Matches 4; Conservative 0; Mismatches 1; Indels
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2 EATTIWGV 9
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2 TAVDAAAI 9
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Peptide a Peptide r Human GAG Peptide e G protein

AAU06698 ADM73347 AAY54566

ABG91199

G protein Cancer-re Human GAG Anti-ELAM Anti-ELAM-ELAM-1 bi ELAM-1 pi ELAM-1 pe ELAM-1 pe Human pro

ABP82665
ADC9257
ADC95257
AAR86049
AAR86065
AAR86065
AAR86065
AAW63859
AAY63859
AAY53859
AAY53859
AAY53859
AAY53859
AAY53859
AAY54722
AAY63859
AAY53859
AAY53859
AAY53859

Adu06698 P
Adm73347 H
Adm73347 H
Adm828265 C
Adc92257 C
Adm86020 H
Aar86002 P
Aar86065 F
Aaw2685 F
Aaw2685 F
Aaw463875 F
Aaw63875 F
Aay67722 P

Peptide a Peptide # Human INT Secreted

Aay67677 Aab61209 1 Abo32652

ALIGNMENTS

Aau38624 Abg91200

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November 14, 2004, 11:57:25 ; Search time 40.5106 Seconds (without alignments) 123.973 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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71
1 TSLDASIIWAMMQN 14
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

seq length: 0 seq length: 23

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Minimum I Maximum I

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
; ; ;	71	100.0	14	<u>_</u> ~	AAY93098	Aav93098 Transform
7	71	100.0	Н	'n	AAY92950	
ю	20	70.4	12	ო	AAY93009	
4	20	70.4	12	m	AAY92947	
'n	50	70.4	12	m	AAY93008	8
9	40	56.3	12	ო	AAY93093	_
7	37	52.1	11	ო	AAY93094	4
89	37	52.1	12	ო	AAY93010	
6	33	46.5	14	4	AAB88161	-
10	31	43.7	21	4	ABG25633	Abg25633 Novel hum
11	30	42.3	15	7	AAR13972	Aar13972 [Asp14]Me
12		42.3	15	7	AAR61463	Aar61463 [Asp-14]
13		40.8	σ	60	ADM73036	Adm73036 Human GAG
. 14	29	40.8	6	æ	ADM73041	Adm73041 Human GAG
15	29	40.8	10	80	ADM73042	Adm73042 Human GAG
16	29	40.8	10	œ	ADM73040	Adm73040 Human GAG
17	29	40.8	10	æ	ADM73035	Adm73035 Human GAG
18	29	40.8	12	m	AAY93007	Aay93007 Transform
19	29	40.8	15	m	AAY54720	
20	29	40.8	15	m	AAY54721	Aay54721 Human sub
21	29	40.8	15	m	AAY67084	Aay67084 Human pro
22	29	40.8	15	m	AAY67083	Human
23	29	40.8	15	4	AAU38622	Aau38622 Human sub
24	29	40.8	15	4	AAU38623	
25	29	40.8	15	'n	ABG91198	Abq91198 Peptide a

RESULT 1 AAY93098	) AAY93098 standard; peptide; 14 AA.		2 AAY93098;		r 08-NOV-2000 (first entry)		Iransforming growth factor inhibitory peptide P144.		! Hepatotropic; antagonist; transforming growth factor betal; TGF-bl;			
RE:	Ω	×	Ϋ́	×	占	×	DΕ	×	₹	₹	Ž	5

WO200031135-A1 Homo sapiens. 02-JUN-2000. 

99WO-ES000375. 98ES-00002465. 23-NOV-1999; 24-NOV-1998; (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA,

Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F; Ezquerro

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Disclosure; Page 31; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGP) factor betal (TGP-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGP-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

Query Match

Best Loc Matches

AAY92950;

RESULT 2 AAY92950

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heparotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor; liver, extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                             Hepatotropic, antagonist, transforming growth factor betal, TGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor, mimetope, cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Borras Cuesta F;
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                                                                                                                                                      Transforming growth factor inhibitory peptide P55.
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                    AAY93009 standard; peptide; 12
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Best Local Similarity
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                                                               AAY93009;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                             'Match 100.0%; Score 71; DB 3; Length 14; Local Similarity 100.0%; Pred. No. 1e-05; les 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor inhibitory peptide #6
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                                                                                                                                                                                                                                                                                                             AAY92950 standard; peptide; 14 AA.
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                         Sequence 14 AA;
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Query Match Local

Best Loc Matches

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RESULT 3

Ezquerro

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGP) factor betal (TGP-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGP-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                      Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 50; DB 3; 75.0%; Pred. No. 0.046;
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Borras Cuesta F;
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                                                                                                                                                                                Disclosure; Page 27; 86pp; Spanish,
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  Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heparotropic, antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Pred. No. 0.046;
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75.0%;
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Best Local Similarity
Matches 9; Conserv
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                                            WO200031135-A1.
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Homo sapiens,
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AAY93008;

RESULT 5 AAY93008

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those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial anino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAV92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatotropic, antagonist, transforming growth factor betal, TGF-b1, competitive inhibition; collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis.
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Pred. No. 2
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TSLDATMIW 9
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Borras Cuesta F;
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                                                                                                                                                                                          Query Match
Best Local Similarity
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Score 37; DB 3; Length 11; Pred. No. 8.4;

52.1%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                         Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Indels
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Pred. No. 9.2;
1; Mismatches
Mismatches
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75.0%;
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Matches 6; Conserv
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us-09-831-253f-6.rag

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food supplement; medical imaging; diagnostic; genetic disorder
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Homo sapiens. 

WO200175067-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73 N-PSDB; AAS89820 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Claim 20; SEQ ID NO 55992; 103pp; English. biodiversity.

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed constant of the constant of

Sequence 21 AA;

Gaps 9 43.7%; Score 31; DB 4; Length 21; 42.1%; Pred. No. 1.9e+02; tive 2; Mismatches 3; Indels Query Match
Best Local Similarity 42.1.
8; Conservative

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1 TSLD-----ASIIWAMMQ 13

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Gaps

AAR13972 standard; protein; 15 AA. AAR13972; AAR13972 

RESULT 11

(revised) 25-MAR-2003 27-NOV-1991

[Asp14]Melittin-(7-21) (5).

Bioassay; immunoassay; polystyrene; polyethylene; sheet; carrier; support; solid-phase

CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; angiogenesis. 25-AUG-2000; 2000WO-US023482. 99US-0150791P. 17-MAY-2001 (first entry) CD66 peptide CD66f(11)-10. Skubitz KM, Skubitz APN; (SKUB/) SKUBITZ K M. (SKUB/) SKUBITZ A P N. WPI; 2001-234981/24. WO200113937-A1. 26-AUG-1999; 02-SEP-1999; 01-MAR-2001 

Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of Cp66 polypeptides, and modulating immune cell activation.

Claim 1; Page 54; 102pp; English.

The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ilgands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one cD66 family polypeptide and/or at least one ligand of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of F-cells, not beterotypic adhesion and/or differentiation of Epithelial cells, homotypic and/or heterotypic adhesion and or heterotypic adhesion and conference of the peptides and adhesion of CD66 family polypeptides to other ligands. The peptides and adhesion of calivering a therapeutically active agent to a patient, for useful for delivering at hemapeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or almoure cells, for altering angiogenesis by contacting endothelial cells, tumoure for its ligand, for altering angiogenesis by immune response, and for altering keratinocyte proliferation

Sequence 14 AA;

ö Score 33; DB 4; Length 14; 2; Indels Pred. No. 55; 2; Mismatches 46.5%; 6; Conservative Query Match Best Local Similarity Matches 6; Conserv

2 SLDASIIWAM 11

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ABG25633 standard; protein; 21 AA. RESULT 10

ABG25633;

18-FEB-2002 (first entry)

ZXEXEXEX ZXEXEXEX

Novel human diagnostic protein #25624.

Human; chromosome mapping; gene mapping; gene therapy; forensic;

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1 TSLDASIIW 9
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                         WPI; 1995-030351/04
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Best Local Similarity
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        Holm A,
                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004022709-A2
                                                                                                                                                                 Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-2004.
                                                      high yields
                                            substrate
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
         RH,
                                                                                                                                                                                                                                                                                                      ADM73036;
         Berg
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                            ADM7303
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                                                                                                                                                                                                                   Protected melittin-(7-21) and twelve analogs (AAR13969-79) derived by substitutions in position 12 and 14 were each assembled stepwise on a labelled sheet. The sheet was an aminomethylated 285$ polystyrenegrated beheet. The sheet labelled by graphite-based ink. The common steps of deprotection, neutralisation, washing and coupling of identical amino acids were performed simultaneously in a single reaction vessel, while the coupling of different amino acids was carried out in separate vessels. The polymer substrate serves as an efficient solid-phase carrier on which the peptide may be synthesised or attached and remain covalently bound in a stable, permanent manner. The resulting support can be used in solid-phase bloassays, esp. (updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                Polymer substrate with grafted polystyrene chains - functionalised to attach aminoacid(s), peptide(s) or proteins, for peptide synthesis, bio-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide solid phase synthesis; polystyrene-grafted substrate; melittin.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 2; Length 15;
Pred. No. 2e+02;
0; Mismatches 3; Indels
                                                                                                                              Holm A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [Asp-14] melittin-(7-21) analogue.
                                                                                                                              Pedersen W,
                                                                                                                                                                                                    Disclosure; Fig 3; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR61463 standard; peptide; 15
                                                                                                 FORSKNINGSCENTER
FORSKNINGSCENTER
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89US-00398846.
92US-00882059.
                                                             90DX-00000559
                                                                                90DK-00000559
                                                                                                                                                                                                                                                                                                                                                         42.3%;
ilarity 66.7%;
Conservative
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                                                                                                                            Almdal K,
                                                                                                                                              WPI; 1991-281427/38
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                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                  immunoassays.
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                                                                                                 (RISO-) RISOE
(RISO-) RISOE
                                                              02-MAR-1990;
                                                                                02-MAR-1990;
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12-MAY-1992;
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                         WO9113098-A
                                                                                                                                                                                                                                                                                                                                          Sequence 15
                                           05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5373053-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-1994
       Synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                            Berg RH,
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Matches
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The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-13 amino acids (SEQ ID NO:108-610); (b) an epitope cluster comprising the polypeptide of (a); (c) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a) - (c); or (e) a nucleic acid encoding the polypeptide of (a) - (l) in a viruoleic acid encoding the early polypeptide of (a) - (l) has viruoleic and cytostatic activities, and can be used in vaccines. The methods and compositions of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitope, epitope cluster, virucide, cytostatic, vaccine, viral infection, cancer; tumour; human, GAGE-1.
                                                                                                                                                                                                                                                                                                                     The invention relates to a solid phase peptide synthesis method using a support consisting of a functionalised polystyrene-grafted polymer substrate. The peptides are prepared in high yield and purity. The process may be used for compartmentalised synthesis of a number of different peptides in parallel. The present sequence is one of 13 melittin. (7-21) analogues prepared in parallel by the process (AAR61460-R61470)
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                                                                                                                                                 grafted with polystyrene - used in peptide synthesis giving
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   Almdal
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Merrifield RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 2;
Pred. No. 2e+02;
0; Mismatches
   Pedersen WB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human GAGE-1 epitope SEQ ID NO:295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM73036 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                          Example 9; Fig 3; 20pp; English
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   Tam JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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epitope, epitope cluster, virucide, cytostatic, vaccine, viral infection, cancer, tumour, human, GAGE-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 301; 357pp; English.
                                                                                                                                                                                                                             Human GAGE-1 epitope SEQ ID NO:301,
                                                                                 ADM73042 standard; peptide; 10 AA.
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                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                            03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitope, epitope cluster, virucide, cytostatic, vaccine, viral infection, cancer, tumour, human, GAGE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral
invention are useful for the diagnosis and/or treatment of viral infections, cancers and tumours. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                     Gaps
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Pred. No. 1.7e+06;
2; Mismatches 2; Indels
                                                                                                                                                                                                2; Indels
                                                                                                                                                      Length 9;
                                                                                                                                              Query Match 40.8%; Score 29; DB 8; I Best Local Similarity 50.0%; Pred. No. 1.7e+06; Matches 4; Conservative 2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human GAGE-1 epitope SEQ ID NO:300.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                  Sequence 9 AA;
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Liu L,

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The present invention describes a polypeptide (I) comprising a component selected from: (a) a polypeptide epitope having any of the 503 fully defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope cluster comprising the polypeptide of (a); (c) a polypeptide having substantial similarity to (a) or (b); (d) a polypeptide having functional similarity to any of (a) c(b); or (e) a mucleic acid encoding the polypeptide of (a) -(d). (T) has virucide and cytostatic activities, and can be used in vaccines. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of viral infections, cancers and tumours. The present sequence is used in the exemplification of the present invention.
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7 IIWAMMQN 14

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Sequence 29, Appl
Sequence 1855, Ap
Sequence 620, Appl
Sequence 620, Appl
Sequence 1844, Ap
Sequence 580, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 2188, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 27, Appl
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                                                                                     November 14, 2004, 13:04:13; Search time 23.3333 Seconds (without alignments) 42.633 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-463-239-29
US-09-139-0430-1855
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US-09-239-0430-1944
US-09-239-0430-1867
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US-09-239-0430-188
US-09-239-0430-188
US-09-239-0430-2188
US-09-239-0430-2188
US-09-239-0430-218
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US-08-336-618-2
                                                                                                                                                                                                                                              478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
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Maximum DB seq length: 15
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Perfect score:
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28 25 32.5 12 4 US-09-389-956-52 Sequence 52, Appl 29 25 32.5 15 1 US-08-049-783-11 Sequence 11, Appl 31 25 32.5 15 1 US-08-316-322 Sequence 22, Appl 32 25 32.5 15 1 US-08-316-322 Sequence 22, Appl 33 25 32.5 15 1 US-08-316-322 Sequence 22, Appl 34 25 32.5 15 2 US-08-611-928-22 Sequence 22, Appl 35 25 32.5 15 3 US-09-173-891-22 Sequence 22, Appl 36 25 32.5 15 3 US-09-173-891-22 Sequence 22, Appl 36 25 32.5 15 3 US-09-076-137-23 Sequence 23, Appl 36 25 32.5 15 4 US-09-173-831-23 Sequence 23, Appl 37 25 32.5 15 4 US-09-514-245-151 Sequence 23, Appl 40 25 32.5 15 4 US-09-514-245-152 Sequence 152, Appl 40 25 32.5 15 5 PCT-US92-03624-23 Sequence 23, Appl 41 25 32.5 15 5 PCT-US92-03624-23 Sequence 23, Appl 42 31.2 13 US-08-290-919-15 Sequence 14, Appl 44 31.2 13 US-08-798-897-14 Sequence 14, Appl 45 24 31.2 14 US-08-798-897-14 Sequence 14, Appl 44 Pept 45 31.2 14 US-08-798-823-14 Sequence 14, Appl 45 24 31.2 14 US-08-798-823-14 Sequence 14, Appl 45 24 31.2 14 US-08-798-823-14 Sequence 14, Appl 45 24 31.2 14 US-08-798-823-14
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APPLICANT: JESTIN, Andre
APPLICANT: JESTIN, Andre
APPLICANT: Le CANN, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: Le CANN, Pierre
APPLICANT: HUTET, Evelynibe
APPLICANT: HUTET, Evelynidue
APPLICANT: ANANULD, Claire
APPLICANT: MAMBE, Dominique
APPLICANT: MAMBE, Dominique
APPLICANT: MAMBE, Dominique
APPLICANT: MAMBE, Dominique
APPLICANT: MAMBE, Evelynidue
APPLICANT: MAMBE, Evelynidue
APPLICANT: MAMBE, 1970,104
APPLICANT: MAMBE, 1970,104
APPLICANT: MAMBE, 1970,104
APPLICANT: MAMBE, 1971,15396
FILE REFERENCE: 1971,15396
FRIOR APPLICATION NUMBER: FR 97/15396
FRIOR APPLICATION NUMBER: FR 97/15396
FRIOR APPLICATION NUMBER: 170
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: TYPE: TT
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ALIGNMENTS
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US-09-514-245-98
US-09-514-245-98
US-09-514-245-98
Sequence 98, Application US/09514245
Fatent No. 6703023
GENERAL INFORMATION:
APPLICANT: ALBINA, Emanuel
APPLICANT: ALE CANN, Flarre
APPLICANT: BLANCHARD, Philipe
APPLICANT: HUTET, Evelyne
APPLICANT: HUTET, Evelyne
APPLICANT: TRUONG, Claire
APPLICANT: TRUONG, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-09-514-245-55
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Best Local Similarity 35.7%;
Matches 5; Conservative
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2 VNELRFNIGQFLPP 15
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APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVINUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
FILE REPERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR APPLICATION NUMBER: 1997-112-05
NUMBER OF SEQ ID NOS: 1770
SOFTWARE: Patentin version 3.0
SEQ ID NO 99
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Sequence 29, Application US/09463239

Sequence 29, Application US/09463239

GENERAL INFORMATION:

APPLICANT: General Anarcus

APPLICANT: Sonnewald, Uwe

TILLE OF INVENITION: Genetic Method for Controlling Sprouting

TILLE OF INVENITION UNMBER: DO 01-21

PRIOR PELLING DATE: 10946-07-10

PRIOR PELLING DATE: 1997-07-10

PRIOR APPLICATION NUMBER: EP 97113118.0

PRIOR PILING DATE: 1997-07-10

SEQ ID NOS: 39

SOFTWARE: Patentin Version 3.0

SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-99
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Southwood, Scott
Vitiello, Maria A.
Livingston, Brian D
Celis, Esteban
Kubo, Haph T.
Grey, Howard M.
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GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitiello, Maria A.
APPLICANT: Livingston, Brian I.
APPLICANT: Livingston, Brian I.
APPLICANT: Kubo, Ralph T.
APPLICANT: Gelis, Esteban
APPLICANT: Gelis, Esteban
APPLICANT: Grey, Howard M.
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                                                                                                                                                                                                                              CARIOLET, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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LRFNIGQFLPP 11
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Matches 5; Conserv
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Best Local Similarity
Matches 6; Conserv
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US-09-239-043D-1855
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US-09-463-239-29
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...relCANT: MAHE, Dominique

APPLICANT: CARIOLET, Roland
APPLICANT: CARIOLET, Roland
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/99/514,245
CURRENT PILING DATE: 2000-02-28
FRIGN APPLICATION NUMBER: FR 97/15396
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO 98
TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE
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US-08-753-750B-64
; Sequence 64, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo. Regide Y.C.
; APPLICANT: Lo. Regide Y.C.
; APPLICANT: BOLTER, Anthony B.
; TITLE OF INVENTION: TRANSFRRILA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753, 750B
; CURRENT APPLICATION NUMBER: C0/108, 569
; PRIOR FILING DATE: 1995-12-01
; PRIOR FILING DATE: 1995-12-01
; PRIOR FILING DATE: 1995-12-01
; SEQ ID NOS: 68
; SEQ THANE: FasteSEQ for Windows Version 4.0
; SEQ ID NO 64
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US-09-514-245-99
US-09-514-245-99
Sequence 99, Application US/09514245
Patent No. 6703023
GENERAL INFORMATION A
APPLICANT: JESTIN, Emanuel
APPLICANT: ALBINA, Emanuel
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ALBIRA, Emanuel
Le CANN, Pierre
BLANCHARD, Phillipe
HUTET, Evelyne
ARNAULD, Claire
TRUONG, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-98
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Best Local Similarity 35.7%;
Matches 5; Conservative
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SESWELGLY 12
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Matches 6; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: SIGNAY, JOHN
APPLICANT: SIGNAY, JOHN
APPLICANT: SIGNAY, JOHN
APPLICANT: Vitiello, Maria A.
APPLICANT: Vitiello, Maria A.
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Chesnut, Robert
APPLICANT: Bipmenner inc.
ITILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
ITILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILING DATE: 1999-01-27
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1994-01-13
PRIOR FILING DATE: 1994-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 3; Length 10;
Pred. No. 55;
4; Mismatches 0; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 184.762
FELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-239-043D-620
; Sequence 620, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LGLYLSPH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||::|:|:
2 LGIHLNPN 9
                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-159-339A-458
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Fatent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: Ubes
NUMBER OF SEQUENCES: 1254
CORRESPONDERS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Orthohepadnaviridae hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/159,339A FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LGLYLSPH 15
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1 LGIHLNPN 8
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Sidney, John
Southwood, Scott
Vitiello, Maria A.
Livingston, Brian D.
Celis, Egteban
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2 LGIHLNPN 9
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Matches 4; Conserv
         2 LGIHLNPN
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US-09-239-043D-580
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APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

FILE REPERENCE: 2060.0060007

CURRENT APPLICATION NUMBER: US 09/189,702

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR APPLICATION NUMBER: US 08/978,291

PRIOR APPLICATION NUMBER: US 08/920,360

PRIOR APPLICATION NUMBER: US 08/013,363

PRIOR PILING DATE: 1997-01-12

PRIOR APPLICATION NUMBER: US 08/41,603

PRIOR PILING DATE: 1995-06-05

PRIOR PILING DATE: 1994-11-20

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR PILING DATE: 1994-12-01

PRIOR PILING DATE: 1994-12-01

PRIOR PILING DATE: 1994-07-21

PRIOR PILING DATE: 1994-07-21

PRIOR PILING DATE: 1994-07-21

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR APPLICATION NUMBER: US 08/
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                                                                                                                                                                                                                                                                                                                                                              Gaps
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 10
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                                                                                                                                                                                                                                                                                         Score 27; DB 4; Length 10;
Pred. No. 55;
4; Mismatches 0; Indels
                                                                                                                                                             TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
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Sequence 1944, Application US/09239043D
Patent No. 6689363
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Vitiello, Maria A.
Livingston, Brian D.
Celis, Esteban
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. boccast
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
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Grey, Howard M.
Chesnut, Robert
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2 LGIHLNPN 9
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8 LGLYLSPH 15

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PRIOR FILING DATE: 1996-03-13
PRIOR PILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/461,603
PRIOR PILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR PILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR PILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PILING DATE: 1994-02-16
PRIOR PILING DATE: 1994-02-16
PRIOR PILING DATE: 1994-02-16
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR APPLICATION ADDICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE PRAISED FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08102738
Patent No. 5674676
GENERAL INFORMATION:
APPLICANT: Seidel, Christoph; Wienhues, Ursula-Henrike;
APPLICANT: Bayer, Hubert; Jung, Guenther-Gerhard; Ihlenfeldt, Hans-APPLICANT: Georg
TITLE OF INVENTION: Determining HCV
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.1%; Score 27; DB 4; Length 11; 50.0%; Pred. No. 62;
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orthohepadnaviridae hepatitis B virus
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,738
FILING DATE: 6-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: DE 42 26 093.0
FILING DATE: 7-AUG-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: DE 42 40 980.2
FILING DATE: 5-DEC-1992
ATTORNEY/AGENT INPORMATION:
NAME: TSA1, Christine H:
NAME: TSA1, Christine H:
NAME: TSA1, Christine H:
NAME: Christine H:
NAME: TSA1, Christine H:
NAME: TSA1, Christine H:
NAME: TSA1, Christine H:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LGLYLSPH 15
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3 LGIHLNPN 10
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US-08-102-738-20
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1867
LENGTH: 11
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                                                                                    TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
CURRENT APPLICATION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR APPLICATION NUMBER: US 08/920,360
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1995-06-05
PRIOR PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR PRIOR PRIOR DATE: 1994-07-21
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APPLICANT: Celis, Esteban
APPLICANT: Chesnut, Robert
APPLICANTON: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REPREBRUE: 2060-0060007
CURRENT PILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR APPLICATION NUMBER: US 08/920,360
PRIOR FILING DATE: 1997-03-12
PRIOR PILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 06/013,363
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NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 62;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
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Southwood, Scott
Vitiello, Maria A.
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
          Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LGIHLNPN 10
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SEQ ID NO 2188
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APPLICANT:
APPLICANT:
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                                                                                                                                        Score 27; DB 1; Length 15; Pred. No. 91; 3; Indels 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 35.1%; Score 27; DB 4; Length 15; Best Local Similarity 50.0%; Pred. No. 91; Matches 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Sequence 264, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 9411-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FEASESQ for Windows Version 2.0

CURRENT APPLICATION DATA:

PILING DATE: 21-Jan-1998

CLASSIFICATION: ONDER: US/09/009,953

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 264:
US-09-0953-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                        Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO:
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JENGTH: 15 amino acids
                                                                                                                                                                                                                           4 LSFQLGLYLSPH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                  4 LAAGVGIYLLPN 15
               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                  US-09-009-953-264
                                                                                                   US-08-102-738-20
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8 LGLYLSPH 15 ||::|:|: 7 LGIHLNPN 14

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APPLICANT: Kubo, Ralph T.
APPLICANT: Kubo, Ralph T.
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: Chesnut, Robert
APPLICANT: Defented and Nucleic Acid Compositions
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FRICK REPERANCE: 1990-01-27
FRICK REPERANCE: 1998-11-10
FRICK APPLICATION NUMBER: US 08/189,702
FRICK APPLICATION NUMBER: US 08/820,360
FRICK APPLICATION NUMBER: US 08/820,360
FRICK APPLICATION NUMBER: US 08/461,603
FRICK APPLICATION NUMBER: US 08/461,603
FRICK APPLICATION NUMBER: US 08/347,610
FRICK FILING DATE: 1994-11-23
FRICK FILING DATE: 1994-11-23
FRICK FILING DATE: 1994-00-01
FRICK FILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 4;
Pred. No. 91;
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US-09-239-043D-2188

; Sequence 2188, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:
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50.0%;
                                                                                                                                                                                                                                                                                                                                  Livingston, Brian
Celis, Esteban
                                                                                                                                                                                                                                                 Southwood, Scott
Vitiello, Maria A.
                                                                                                                                                                 Sette, Alessandro
Sidney, John
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Best Local Similarity 50.0
Matches 4; Conservative
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LGIHLNPN 14
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RESULT 2
US-10-682-420-55
Sequence 55, Application US/10682420
Publication No. US20040062775A1
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
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SLTFQLLLFL 10
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RESULT 1
US-09-572-270A-102
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98, Appl
98, Appl
98, Appl
55, Appl
26, Appl
101, App
757, App
                                                                                                   November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds (without alignments) 66.619 Million cell updates/sec
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1: \cgn2 \( \) \cgn\( \) \c
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-682-420-55
US-10-682-420-98
US-10-409-613-98
US-10-442-180-98
US-10-442-180-98
US-10-197-554-26
US-10-197-554-26
US-10-601-953-60
US-10-601-953-60
US-10-601-953-60
US-10-322-266-758
US-10-322-266-758
US-10-322-266-758
US-10-322-266-758
US-10-322-266-758
US-10-322-266-758
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Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in ILL2. at 8-17 and may interact with
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Publication No. US20030148368A1

GENERAL INFORMATION:

APPLICART: Proteom Ltd

TITLE OF INVENTION: Inter- complementary peptide listing
FILE REFRENCE:

CURRENT APPLICATION NUMBER: US/09/572,270A

UNMBER OF SEQ ID NOS: 1144

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 102

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                    40.3%; Score 31; DB 10; Length 10; 70.0%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
US-10-191-540-154
US-10-302-100B-34
US-10-199-820-274
US-10-081-119-28
   45554006455444499999999944444
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Best Local Similarity 70.0
Matches 7; Conservative
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TYPE: PRT
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                                                                                    APPLICANT: MAHE, DOMINIQUE
APPLICANT: MAHE, DOMINIQUE
APPLICANT: MAHE, DOMINIQUE
APPLICANT: MAHE, DOMINIQUE
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISBASE (PWD)
FILE REPERBENCE: 065691/0176
CURRENT FILING DATE: 2003-10-10
FRIOR APPLICATION NUMBER: US/10/637,011
FRIOR APPLICATION NUMBER: US/09/514,245B
FRIOR APPLICATION NUMBER: WS/09/514,245B
FRIOR PILING DATE: 2000-02-28
FRIOR PELING DATE: 2000-02-28
FRIOR PELING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE PACENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ARNAULD, CLAILE
APPLICANT: ARNAULD, CLAILE
APPLICANT: TRUONG, CACHEAINE
APPLICANT: TRUONG, CACHEAINE
APPLICANT: CARIOLET, ROland
APPLICANT: CARIOLET, ROland
APPLICANT: CARIOLET, ROland
APPLICANT: CARIOLET, FOR CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PWD)
TITLE OF INVENTION: DISEASE (PWD)
TITLE OF INVENTION: UNMER: US/10/632,420
CURRENT APPLICATION NUMBER: US/10/637,011
PRIOR PLILING DATE: 2003-10-10
PRIOR PLILING DATE: 2003-08-08
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARRE: PARENTIN VERSION 3.0
SOFTWARRE: PARENTIN VERSION 3.0
SEQ ID NO 98
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 15; Length La Pred. No. 2.8e+02; Sred. No. 2.8e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 98, Application US/10682420 Publication No. US20040062775A1 GENERAL INFORMATION: Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALBINA, Emanuel
Le CANN, Pierre
BLANCHARD, Phillipe
HUTET, Evelyne
ARNAULD, Claire
TRUONG, Catherine
BLANCHARD, Phillipe
HUTET, Evelyne
ARNAULD, Claire
TRUONG, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Type A PWD circovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Type B PWD circovirus US-10-682-420-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
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Best Local Similarity 35.7
Matches 5; Conservative
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Gaps

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APPLICANT: ANAMALD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: MAME. Dominique
APPLICANT: MADEC, Francois
APPLICANT: MADEC, Francois
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: CIRCOVIRUS (PWD)
FILE REFERENCE: 065691/0176
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US/09/514,245B
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFFWARE: Patentin version 3.0
SOFFWARE: Patentin version 3.0
SEQ ID NO 98
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: MAHE, Dominique
APPLICANT: MADE, Francois
APPLICANT: MADER: US/10/409,613
FILE REFERENCE: 05699/0176
CURRENT APPLICATION NUMBER: US/09/514,245B
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
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Pred. No. 2.8e+02;
4; Mismatches 5; Indels
                                                                                                                                                       Sequence 55, Application US/10409613; Publication No. US20040076635A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98, Application US/10409613
Publication No. US20040076635A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Type B PWD circovirus US-10-409-613-55
                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: Le CANN, Pierre
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Phillipe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.0%;
Best Local Similarity 35.7%;
Matches 5; Conservative ,
2 VNELRFNIGOFLPP 15
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Gaps

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Sequence 101, Application US/10119536A
Publication No. US20030199438A1
GENERAL INFORMATION:
APPLICANT: Shaw, Allan Christian
APPLICANT: Shaw, Berg
TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteri.
FILE REPREBUCE: 4305/1J091US1
CURRENT APPLICATION NUMBER: US/10/119,536A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Siddiqi, Suhaib
APPLICANT: Siddiqi, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: Compositions
FILE REFERENCE: 24743-2305
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: US/10/197,954
CURRENT FILING DATE: 2001-07-16
PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 14; Length 11; Pred. No. 2.9e+02; Aismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.0%; Score 30; DB 15; Length 15; 35.7%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
   CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT FILING DATE: 2003-05-21
FRIOR APPLICATION NUMBER: US/09/514,245
FRIOR FILING DATE: 2000-02-28
FRIOR APPLICATION NUMBER: FR 97/15396
FRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFWARE: Patentin version 3.0
SEQ ID NO 98
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-10-197-954-26
; Sequence 26, Application US/10197954
; Bublication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K"ster, Hubert
                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-442-180-98
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Matches 5; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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US-10-197-954-26
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APPLICANT: CARIOLET, Roland
APPLICANT: CARIOLET, Roland
APPLICANT: PARABEC, Francoir
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PWD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
APPLICANT: MATE, DOMINICANTICAL
APPLICANT: MATE, DOMINICAL
APPLICANT: MATE, DOMINICANTICAL
APPLICANT: MATE, DOMINICAL
APPLICANT: MATE, DOMINICANT: MATE, DO
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                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                       Score 30; DB 15;
Pred. No. 2.8e+02;
4; Mismatches 5
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CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: US/09/514,245
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR APLICATION NUMBER: PS 97/15396
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 55
TYPE: PRI
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Publication No. US20040091502A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/10442180 Publication No. US20040091502A1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Type B PWD circovirus US-10-442-180-55
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Le CANN, Pierre
BLANCHARD, Philipe
HUTET, Evelyne
ARNAUID, Claire
TRUONG, Catherine
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APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
                                                                                                                                                                    Query Match 39.0%;
Best Local Similarity 35.7%;
Matches 5; Conservative
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TRUONG, Catherine
                                                                                                                                                                                                                                                                                                        1 LDSLSFQLGLYLSP 14
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Gaps

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GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
FILE REFERENCE: NPC10557
CURRENT APPLICATION NUMBER: US/10/322,266
CURRENT FILING DATE: 2002-12-17
SOFTWARE: Petentin version 3.2
SEQ ID NO 758
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                                                                                                                                                                                                      Score 28; DB 15; Length 10;
Pred. No. 4e+02;
3; Mismatches 1; Indels
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TITLE OF INVENTION: 83 Human Secreted Proteins
FILE REPRENCE: PSO12F1
CURRENT APPLICATION NUMBER: US/09/820,649
CURRENT FILING DATE: 2001-03-30
FRICA APPLICATION NUMBER: US/09/236,557
FRICA APPLICATION NUMBER: PCT/US98/15949
FRICA PRILING DATE: 1999-01-26
FRICA FILING DATE: 1999-01-26
FRICA FILING DATE: 1997-07-30
FRICA FILING DATE: 1997-07-30
FRICA FILING DATE: 1997-07-30
FRICA REPLICATION NUMBER: 60/054,209
FRICA FILING DATE: 1997-07-30
FRICA REPLICATION NUMBER: 60/054,214
FRICA FILING DATE: 1997-07-30
FRICA REPLICATION NUMBER: 60/054,214
FRICA FILING DATE: 1997-07-30
FRICA FILING DATE: 1997-07-30
FRICA FILING DATE: 1997-07-30
                                                                                                     FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-60
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; OTHER INFORMATION: Synthetic construct
US-10-322-266-758
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; Publication No. US20040115135A1
SEQ ID NO 60
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                         36.4%;
50.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.0
Matches 4; Conservative
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US-10-322-266-758
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Sequence 60, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Unactional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therapeutic Compounds
FILE REFERENCE: 02-03US
CURRENT APPLICATION NUMBER: 12/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: PatentIn version 3.2
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; Sequence 757, Application US/10462452
; Publication No. US20040037809A1
; Publication No. US20040037809A1
; Publication No. US20040037809A1
; APPLICANT: Quay, Steven
; APPLICANT: Gupta, Mallini
; ITLE OF INVENTION: Compositions and Methods for Enhanced
; FILE REFERENCE: 02-0205
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US/10/462,452
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 757
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.4%; Score 28; DB 14; Length 9; Best Local Similarity 71.4%; Pred. No. 1.4e+06; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                             FEATURE:
NAME/KEY: BINDING
LOCATION: (1)..(9)
COTATION: CPN0998 immunogenic peptide
US-10-119-536A-101
  CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: DK PA 200100581
PRIOR FILING DATE: 2001-04-09
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin version 3.1
SEQ ID NO 101
                                                                                                                                                                              TYPE: PRT ORGANISM: Chlamydia pneumoniae
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Best Local Similarity 50.0
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-462-452-757
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2 IGKYLSP 8
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APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISBASE (PWD)
FILE REFERENCE: 065691/0176
FULE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/682,420
CURRENT FILING DATE: 2003-10-10
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Pred. No. 5.7e+02;
3; Mismatches 2; Indels
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PRIOR PILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US/09/514,245B
PRIOR FILING DATE: 2000-02-28
PRIOR PLING DATE: 1997-12-05
PRIOR PLING DATE: 1997-12-05
NUMBER OF SEC ID NOS: 170
SOFTWARE: Patentin version 3.0
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  PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,554
PRIOR PILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,730
PRIOR FILING DATE: 1997-08-19
NUMBER: OF SEQ ID NOS: 353
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 99, Application US/10682420; Publication No. US20040062775A1; GENERAL INFORMATION:
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APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
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; ORGANISM: Type A PWD circovirus
US-10-682-420-99
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.4
Best Local Similarity 50.0
Matches 5; Conservative
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1 LRFNIGQFLPP 11
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5 SISYSIGLVL 14
                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 15
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APPLICANT:
                                                                                                                                                                                                                                                                 TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/054,215
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,211
PRIOR FILING DATE: 1997-07-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 353
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 319
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                        36.4%; Score 28; DB 10; Length 14; 50.0%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 319, Application US/J0160162;
Publication No. US20030166541A1
GERRRAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION:
B3 Human Secreted Proteins
FILE REFERENCE: PS012P2
CURRENT FILING DATE: 2002-06-04
FRIOR APPLICATION NUMBER: US/10/160,162
CURRENT FILING DATE: 2002-06-05
FRIOR APPLICATION NUMBER: O9/236,558
FRIOR APPLICATION NUMBER: O9/236,557
FRIOR APPLICATION NUMBER: 60/054,212
FRIOR APPLICATION NUMBER: 60/054,212
FRIOR APPLICATION NUMBER: 60/054,212
FRIOR APPLICATION NUMBER: 60/054,213
FRIOR PILING DATE: 1997-07-30
FRIOR APPLICATION NUMBER: 60/054,213
FRIOR PILING DATE: 1997-07-30
FRIOR APPLICATION NUMBER: 60/054,214
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FRIOR APPLICATION NUMBER: 60/054,214
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FRIOR APPLICATION NUMBER: 60/054,215
FRIOR FILING DATE: 1997-07-30
FRIOR APPLICATION NUMBER: 60/054,215
FRIOR FILING DATE: 1997-07-30
FRIOR FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SLSFQLGLYL 12
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5 SISYSIGLVL 14
                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-820-649-319
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2004, 12:55:26; Search time 93.3333 Seconds (without alignments) 57.653 Million cell updates/sec Run on:

US-09-831-253F-9 77

1 LDSLSFQLGLYLSPH 15 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_23Sep04:\* Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

u o	Transform	Transform	Arabidops	Human I k	Miniature	Exemplary	Human pep	HCV nonst	HCV nonst	HCV nonst	Human pep	HCV nonst	HCV nonst	HCV nonst	_	Chlamydia	Permeabil	Human cla	Antigenic	Adult I-c	Gene 33 h	Novel hum	Human sec	Python re	Hepatitis
Description	Aay93106	Aay92953	Aaq83462	Abp58975	Aam47809	Adn03302	Aab07274	Abr00682	Abr00699	Abr00693	Aam97619	Abr00703	Abr00706	Abr00715	Abr00714	Abp75290	Adi46351	Adp87353	Aap50351	Aap50388	Aab34406	Add90504	Adg90323	Aae03688	Abi08453
ID	AAY93106	AAY92953	AAG83462	ABP58975	AAM47809	ADN03302	AAB07274	ABR00682	ABR00699	ABR00693	AAM97619	ABR00703	ABR00706	ABR00715	ABR00714	ABP75290	ADI46351	ADP87353	AAP50351	AAP50388	AAB34406	ADD90504	ADG90323	AAE03688	ABJ08453
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Score	77	77	31	31	30	29	29	29			29	29	29	29	29	28		28		28	28	28	28	27	27
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ABJ08063 ADK38987 AAY38160 AAY45728	AAG83460 AAG94985 ABJ06472	ABJ08542 ADK37752 ADK39076	ABJ08090 ABJ08471 ABJ06432	ABJ06307 ABJ08454 ABJ08064	ADK37599 ADK37712 ADK38999
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22 23 24 36 36	321	1 4 13 16 1 4 13 16	33 38 39	4 4 4 0 1 2	4 4 4 5 4 5

## ALIGNMENTS

RESULT 1

Transforming growth factor inhibitory peptide P152. AAY93106 standard; peptide; 15 AA. (first entry) 08-NOV-2000 AAY93106; AAY93106 

Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope, cirrhosis.

Homo sapiens.

WO200031135-A1.

02-JUN-2000.

99WO-ES000375. 23-NOV-1999;

98ES-00002465. 24-NOV-1998; (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Disclosure; Page 33; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth. (TGF) factor betal (TGF-b) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

Matches

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RESULT 2

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The present invention relates to a set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is one such peptide from Arabidopsis thaliana. The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or herbicide. The peptides are also useful for tools for agricultural research and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; I kappa B kinase inhibitor 37.40; recombinant production; gene therapy; cancer; tumour; angiocardiopathy; cardiovascular disorder; neurological disorder; immune disorder; inflammatory condition; cytostatic; antiinflammatory; immunomodulator; N-terminal peptide; enzyme linked immunosorbent assay; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A set of peptide ligands for agricultural research and development of therapeutic agents comprise specific complementary peptides to proteins encoded by genes of plant genomes.
                                                                                                                                                                   Plant; peptide pesticide; peptide herbicide; agricultural research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human I kappa B kinase inhibitor 37.40 N-terminal peptide.
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98;
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                                                                                                                                 Arabidopsis thaliana peptide ligand #102.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 45; 201pp; English.
           AAG83462 standard; peptide; 10 AA.
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                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                     (PROT-) PROTEOM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-381629/40.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                 WO200142279-A2
                                                                                                                                                                                                                                                                                                                                                                 13-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development
                                                                                                                                                                                                                                                                                     14-JUN-2001
                                                     AAG83462;
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AAG83462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGP) factor betal (TGP-1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGP-b1 and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor, liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                             Gaps
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                                                 core 77; DB 3; Length 15; red. No. 5e-07; Mismatches 0; Indels
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Pred. No. 5e-07;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Transforming growth factor inhibitory peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
                                                     Score 77;
Pred. No. E
                                                                                                                                                                                                                                                                 AAY92953 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 82; 86pp; Spanish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Sci
100.0%; Pr
tive 0; 1
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                                                 Match 100.0%;
Local Similarity 100.0%;
les 15; Conservative 0;
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                         1 LDSLSFQLGLYLSPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
             Sequence 15 AA
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                                                                                                                                                                                                                                                                                                       AAY92953;
                                                   Query Match
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AAY92953
XXX AAY5
XXX AAX5
XXX

RESULT 3

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Gaps

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Length 10

5

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The invention relates to an avian pancreatic polypeptide, modified by substitution of at least one amino acid residue, where the residue is being exposed on the alpha helix domain of the polypeptide when the polypeptide is in a tertiary form. The polypeptide is useful for screening drugs to identify agents capable of binding to the same binding site as the avian pancreatic polypeptide. It is also useful for diagnostic purposes to identify the presence and/or detect the levels of DNA or protein that binds to the polypeptide, in treatment of diseases associated with the presence of a particular DNA or protein, where the polypeptide can be used to bind to DNA to promote or inhibit transcription and for identifying binding partners. The present sequence is that of a miniature protein and another molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collection of capture compounds capable of binding to biomolecules to form complexes that are stable under mass spectrometry conditions, useful
modification by substitution of an amino acid residue, that is exposed the alpha helix domain of the polypeptide is useful for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a collection of capture compounds capable of binding to biomolecules to form complexes that are stable under mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide ligand; proteome; capture compound; mass spectrometry;
                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exemplary peptide ligand for proteome analysis #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for analysis of biomolecules, especially proteins
                                                                                                                                                                                                                                                                                                                                                    39.0%; Score 30; DB 5; I
85.7%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN03302 standard; peptide; 11 AA.
                                                              Example 17; Fig 5; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-2002; 2002US-00197954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-2001; 2001US-0306019P.
21-AUG-2001; 2001US-0314123P.
11-MAR-2002; 2002US-0363433P.
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                                                                                                                                                                                                                                                                                                                                                                                                                   6 FQLGLYL 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
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                                 drugs.
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                                                                                                                                                                                                                                               The invention relates to human I kappa B kinase inhibitor 37.40 (ABPSS974) and nucleic acids encoding it (ABZ70827). The protein has a molecular weight of 37.4 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic and the use of the protein, gene and antagonist in therapeutic treatment of a variety of diseases such as cancer, angiocardiopathy neurological disorders, immune disorders and inflammatory conditions. The present sequence represents the 15 N-terminal amino acids of human I kappa B kinase inhibitor 37.40 used in ELISA (enzyme linked immunosorbent assay) in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avian pancreatic polypeptide; alpha helix domain; modulate transcription; miniature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide scaffold e.g. an avian pancreatic polypeptide that comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                       Human inhibitor molecule I kappa B kinase 37.40 polypeptides and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.3%; Score 31; DB 5; Length 15; 75.0%; Pred. No. 1.5e+02; ative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                     Example 5; Page 18 (Disclosure); 33pp; Chinese.
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                                                                                                                                                                                         polynucleotides encoding this polypeptide.
                                                                            (BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM47809 standard; peptide; 15 AA
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Zondlo NJ;
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16-OCT-2000; 2000US-024056FP.
30-JAN-2001; 2001US-026099P.
23-FEB-2001; 2001US-027136BP.
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              26-DEC-2000; 2000CN-00136306
                                            26-DEC-2000; 2000CN-00136306
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Best Local Similarity
6; Conserve
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5 FLLGLYIS 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miniature protein 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
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                                                                                                         Mao Y, Xie Y;
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Gaps

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spectrometry conditions. The formulae for the capture compounds comprises sets of compounds of formula (I)-(III) given in the specification. Also included are analysis of biomolecules (by contacting a composition comprising a biomolecule with the above collection and identifying or detecting bound biomolecules), separating protein conformers (by contacting a composition comprising a biomolecule with the above collection, separating the members of the collection and identifying or contacting the mixture with the above collection and identifying bound proteins), reducing diversity of a complex mixture of biomolecules (by contacting the mixture with the above collection and separating each set of complexes of capture compounds with biomolecules from the other sets) and identifying phenotype-specific biomolecules (by sorting cells from a single subject into sets according to a phenotype, contacting mixtures of biomolecules from each set with the above collection and comparing the patterns of biomolecule binding from each set). The collection of capture compounds is useful for the analysis of contacting mass spectrometry, especially matrix assisted laser desorption ionisation time of flight (Mallol-TOP) mass spectrometry. The present sequence is an exemplate of the above collection of capture capture comporated into a capture is an exemplate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compound of the invention
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37.7%; Score 29; DB 8; Length 11; 60.0%; Pred. No. 2.5e+02; tive 2; Mismatches 2; Indels
                                                                                                                                       AAB07274 standard; peptide; 12 AA.
                           6; Conservative
                                                  1 LDSLSFQLGL 10
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                                                                  Best Local Similarity
Matches 6; Conserv
 Query Match
                                                                                                             RESULT 7
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Human peptido-mimetic # 108.
    (first entry)
    17-OCT-2000
 AAB07274;
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Human; peptido-mimetic; tumour metastasis; E-selectin; adhesion molecule; Lewis antigen; anti-adhesion therapy. Homo sapiens.

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99WO-US026277
                                                                                 98US-0107478P
WO200027420-A1
                                                                              06-NOV-1998;
                                                      05-NOV-1999;
                           18-MAY-2000
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Peptidomimetics of carbohydrate Lewis ligands useful for modulating WPI; 2000-376309/32

(WIST-) WISTAR INST ANATOMY & BIOLOGY.

(UYPE-) UNIV PENNSYLVANIA.

Blaszczyk-Thurin M, Kieber-Emmons T;

Claim 8; Page 58; 107pp; English.

inflammation, metastasis and angiogenesis.

Tumour metastasis requires detachment of malignant cells from the primary tumour, penetration of blood or lymph vessels and attachment to the endochellum of distant organs, ultimately resulting in the formation of new tumours. The selectin family of adhesion molecules is implicated in this process. E-selectin is a calcium-dependent molecule expressed by activated vascular endothelium. E-selectins bind to glycoconjugates

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carrying a terminal tetrasaccharide Lewis antigen, which are found on tumour cell surfaces. One such Lewis antigen is sialyl (SA)-Lea. The binding of selectin molecules to their ligands is thought to be an important step in metastasis. Therefore, inhibition of E-selectindependent carbohydrate-mediated interactions is thought to be a target for anti-cancer therapy. The present sequence is a Human Family II peptido-mimetic of E-selectin-SA-Lea binding. This sequence blocks E-selectin-SA-Lea binding and therefore blocks adhesion of tumour cells a leukocytes to endothelial cells and hence metastasis. This sequence is therefore an E-selectin antagonist
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic; non-structural protein; virucide; gene therapy; immunological; NSSA;
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                                                                                                                                                                                                                                                                  Length 12;
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Pred. No. 2.8e+02;
3; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV nonstructural protein NS5A complementary peptide 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR00682 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                37.7%;
50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                               DSLSFQLGLY 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                            Sequence 12 AA;
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Indels

Pred. No. 3.1e+02; Mismatches

50.0%;

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Best Local Similarity Matches 6; Conserv

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4 LSFQLGLYLSPH

LGFQPGLKVAQH 13

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The invention relates to a novel method for identifying a compound useful for treating Hepatitis C virus (HCV) infection. The method comprises assessing the ability of a candidate compound to interfere with the binding of an amphipathic helix present in the N-terminal region of an HCV non-structural protein with cytoplasmic membranes of a eukaryotic cell, where a compound that interferes with the binding is useful for treating the infection. The compounds of the invention have virucide, and hepatotropic activity. The peptides may have a use in gene therapy. The methods and compounds are useful for treating Hepatitis C virus (HCV) infection. The composition is useful for eliciting an immunological response against HCV. The peptides are useful for the preparation of a medicament for the prevention or treatment of HCV infection in a human. The sequences shown in ABR00595-ABR00746 represent complementary peptides
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The sequences shown in ABR00595-ABR00746 represent complementary peptides of varying lengths to the amphipathic helix of the HCV nonstructural protein NS5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a compound for treating Hepatitis C virus (HCV) infection by assessing the ability of a compound to interfere the binding of an amphipathic helix of an HCV nonstructural protein with cytoplasmic membranes of eukaryotic cell.
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
non-structural protein; virucide; gene therapy; immunological; NS5A;
complementary peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV nonstructural protein NS5A complementary peptide 105.
                                                                                                                           Length 12;
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                                                                                                                         Score 29; DB 6; I
Pred. No. 2.8e+02;
2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glass JI;
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                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                         LGFQPGLKVAQH 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
                                                                                        Sequence 12 AA;
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HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic; non-structural protein; virucide; gene therapy; immunological; NSSA;

complementary peptide.

Hepatitis C virus. WO200289731-A2. Glass JI

Glenn JS, Myers TM, WPI; 2003-201229/19.

(STRD ) UNIV STANFORD. (ELIL ) LILLY & CO ELI

03-MAY-2002; 2002WO-US013951 03-MAY-2001; 2001US-0288687P. 31-AUG-2001; 2001US-0316805P.

14-NOV-2002.

HCV nonstructural protein NS5A complementary peptide 99.

01-APR-2003 (first entry)

ABR00693;

ABR00693 standard; peptide; 13 AA.

RESULT 10 ABR00693

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a compound for treating Hepatitis C virus (HCV) infection by assessaing the ability of a compound to interfere the binding of an amphipathic helix of an HCV nonstructural protein with cytoplasmic membranes of eukaryotic cell.
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Matches 6
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37.7%; Score 29; DB 6; Length 13;

Sequence 13 AA;

Query Match

us-09-831-253f-9.closed.rag

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(first entry)

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Identifying a compound for treating Hepatitis C virus (HCV) infection by assessing the ability of a compound to interfere the binding of an amphipathic helix of an HCV nonstructural protein with cytoplasmic
                                                                                                                                                                             HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic; non-structural protein; virucide; gene therapy; immunological; NS5A; complementary peptide.
                                                                                                                                     HCV nonstructural protein NS5A complementary peptide 109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 44; Page 14; 43pp; English.
ABR00703 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membranes of eukaryotic cell.
                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-2002; 2002WO-US013951.
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                                            ABR00703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to oligomucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, anglopoletin, apoptosis related proteins, cadherin, cyclin, proteins, complement related proteins, cyclochromes, kinesins, cytokines, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligomucleotide. The oligomucleotides and the peptide encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with the prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthitis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms
                                                                                                                                                                                                                                              Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; elemeuroprotective; antinicrobial; gene therapy; vaccine; amqlase; cancer; amyloid protein; andiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; d-protein coupled receptor; thiosesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 29; DB 4; Length 14; 46.2%; Pred. No. 3.3e+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                    Human peptide #894 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 3863; 4143pp; English.
                                                               AAM97619 standard; peptide; 14 AA.
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                          (first entry)
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                                                                                                          24-JAN-2002
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                                                                                                             AAM97619;
                  RESULT 11
                                            AAM97619
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Glass JI;

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The invention relates to a novel method for identifying a compound useful for treating Hepatitis C virus (HCV) infection. The method comprises assessing the ability of a candidate compound to interfere with the binding of an amphipathic helix present in the N-terminal region of an C HCV non-structural protein with cytoplasmic membranes of a eukaryotic cell, where a compound that interferes with the binding is useful for treating the infection. The compounds of the invention have virucide, and hepatotropic activity. The peptides may have a use in gene therapy. The methods and compounds are useful for treating Hepatitis C virus (HCV) infection. The composition is useful for eliciting an immunological cespones against HCV. The peptides are useful for the preparation of a medicament for the prevention or treatment of HCV infection in a human. The sequences shown in ABR00595-ABR00746 represent complementary peptides of varying lengths to the amphipathic helix of the HCV nonstructural
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Pred. No. 3.3e+02;
2; Mismatches 4; Indels
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RESULT 12 ABR00703

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The invention relates to a novel method for identifying a compound useful for treating Hepatitis C virus (HCV) infection. The method comprises assessing the ability of a candidate compound to interfere with the binding of an amphipathic helix present in the N-terminal region of an C HCV non-structural protein with cytoplasmic membranes of a eukaryotic cell, where a compound that interferes with the binding is useful for treating the infection. The compounds of the invention have virucide, and chapatotropic activity. The peptides may have a use in gene therapy. The methods and compounds are useful for treating Hepatitis C virus (HCV) infection. The composition is useful for eliciting an immunological composition is useful for eliciting an immunological medicament for the prevention or treatment of HCV infection in a human. The sequences shown in ABR00595-ABR00746 represent complementary peptides
                                                                                                                                                                                                                                                                                                                                                             Identifying a compound for treating Hepatitis C virus (HCV) infection lassessing the ability of a compound to interfere the binding of an amphipathic helix of an HCV nonstructural protein with cytoplasmic
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Pred. No. 3.6e+02;
2; Mismatches 4; Indels
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                                                                                                                                 03-MAY-2001; 2001US-0288687P. 31-AUG-2001; 2001US-0316805P.
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                     HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic; non-structural protein; virucide; gene therapy; immunological; NS5A;
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Pred. No. 3.3e+02;
2; Mismatches 4; Indels
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Best Local Similarity 50.0%;
Matches 6; Conservative ;
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                                                                  complementary peptide
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                                                                                                          Hepatitis C virus.
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RESULT 14 ABR00715

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PR 31-AUG-2001; 2001US-0316805P.

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(STRD ) UNIV STANFORD.

PA (ELIL ) LILLY & CO ELI.

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Glenn JS, Myers TM, Glass JI;

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Oy 4 LSFQLGLYLSPH 15

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Db 2 LGFQPGLKVAQH 13

Search completed: November 14, 2004, 13:11:18
Job time: 94.3333 Becs

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Query Match 37.7%; Score 29; DB 6; Length 15; Best Local Similarity 50.0%; Pred. No. 3.6e+02; Matches 6; Conservative 2; Mismatches 4; Indels

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TISSUE-Skin secretion;
MEDLINE-97368637; PubMed=9255251;
MEDLINE-97368637; PubMed=9255251;
MEDLINE-97368637; PubMed=9255251;
MEDLINE-97368637; PubMed=9255251;
MEDLINE-97368637; PubMed=9255251;
MEDLING-1000 the franchin peptides from the skin secretion of the giant tree frog Litoria infrafrenata.";
J. Pept. Sci. 2:117-124(1996).
J. PUBCILOUAN Ge spectrum antimicrobial peptide.
J. SUBCELLULAR LOCATION: Secreted.
J. SUBCELLULAR EXPRESSED by the skin parotoid and/or rostral.
                                                                                                                                                                                                                                                                                                                                                                                                                 glands.
-!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.
Amidation; Amphibian defense peptide; Antibiotic;
Direct protein sequencing.
MOD RES 12 Leucine amide.
                                                                                                                                                                                                                                                            Litoria infrafrenata (Giant tree frog).
Wasaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae; Pelodryadinae, Litoria.
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P93966
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16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Acid shock protein 1 (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfranciscensis Lactobacillus sanfranciscensis (Lactobacillus sanfranciscensis Lactobacillus sanfranciscensis (Lactobacillus sanfranciscensis).
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Pred. No. 8.9e+02;
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                                                                                                                                                                                                                        Created)
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70.0%;
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Matches 7; Conservative
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NCBI_TaxID=61195;
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FRE1 LITIN
ID FRE1 LITIN
AC P82021;
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 [1] SEQUENCE.
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Q7m3g3 bos taurus
P92702 cubadra her
Q91252 bos taurus
P6256 litoria chl
P6256 litoria spl
P6251 litoria spl
Q61dpB pseudomona
Aaa26012 pseudomon
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P92211
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P92384
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                       1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                        FRE1_LITIN
ASP1_LACSN
Q9R4T0
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P92072
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Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length
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Maximum DB seq length: 15
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Perfect score:
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Eukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Sigmurethra, Helicoidea, Bradybaenidae, Euhadra.
NCBI_TaxID=58912,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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MEDLINE=95403474; PubMed=7673255;

Cardozo C., Bleuteri A.M., Orlowski M.;

Cardozo C., Bleuteri A.M., Orlowski M.;

Differences in catalytic activities and subunit pattern of multicatalytic proteinase complexes (proteasomes) isolated fropituitary, lung, and liver. Changes in LMP7 and the component necessary for expression of the chymotrypsin-like activity.";

J. Biol. Chem. 270:22645-22651(1995).

SEQUENCE 15 AA; 1640 MW; DB334789F42EB2DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Hepatopancreas;
Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
Watanabe K., Thomas R.H.;
Submitted (MaY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z71697; CAA96373.1; --
GO, GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMP7 multicatalytic proteinase complex subunit (Fragment).
Bos taurus (Bovine).
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Pred. No. 6.1e+03;
5; Mismatches 3; Indels
                                                    Length 15;
                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.9%; Score 23; DB 2; Length 9; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels
6358BCB0D3627321 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                               DB 2;
                                               Score 24; DB 2
Pred. No. 4e+03
5; Mismatches
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30.8%;
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15 AA; 1710 MW;
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DSIDYRKKGYVTP 15
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Best Local Similarity 27.3
Matches 3; Conservative
                                                                                                      4; Conservative
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                                                                          Sest Local Similarity
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NCBI_TaxID=9913;
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SEQUENCE
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Matches
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Q9TR52
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                                                                                                                                                                                                                                                                                                                   Gaps
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                                               De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M., "The acid-stress response in Lactobacillus sanfranciscensis CBl."; Microbiology 147:1863-1873(2001).
--- INDUCTION: Overexpressed in acid environments.
Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28K serine proteinase homolog (Fragment).
Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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Ho P.L., Carpenter M.R., Smillie L.B., Gambarini A.G.;
"Co-purification of proteases with basic fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
Periplasmic protein 5 (Fragment).
Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhodobacteraese; Rho
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Pred. No. 2.6e+03;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                            Score 26; DB 1; Length 15; Pred. No. 1.7e+03;
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                                                                                                                                                                                                             575853B4DFB030A8 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                   MEDLINE=21322712; PubMed=11429463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anaerobic or aerobic condition.";
Arch. Microbiol. 162:335-343(1994)
SEQUENCE 15 AA; 1718 MW; DASBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95160605; PubMed=7857198;
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15 AA; 1509 MW;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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4 DSETFQSGM 12
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SEQUENCE
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RESULT 3 Q9R4T0

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Pelodryadinae; Litoria.
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Best Local Similarity
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A Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;

The wantibiotic caerin 1 peptides from the skin secretion of the australian tree frog Litoria caloris. Comparison of the activities of the caerin 1 peptides from the genus Litoria.";

L. Pept. Res. 5:1.21-126(1998).

- PUNCTION: Caeridins show neither neuropeptide activity nor antibiotic activity.

- PUNCTION: Caeridins show neither neuropeptide activity nor antibiotic activity.

- TISSUE SPECIFICITY: Secreted by the skin.

- TISSUE SPECIFICITY: Secreted by the Asp-4 residue in caeridin 1.2; a cyclic succiniminde may be formed between Asp-4 and Gly-5 residues in caeridin 1.3 (By similarity).

A Amidation; Amphibian defense peptide; Direct protein sequencing.

MOD RES 12 Leucine amide.

SEQÜENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waugh R.J., Steinborner S.T., Bowie J.H., Wallace J.C., Tyler M.J., Hu P., Gross M.L., "Two isomeric alpha and beta aspartyl dodecapeptides and their cyclic amino succinyl analogue from the Australian tree frog Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND MASS SPECTROMETRY.

TISSUE=Parotoid gland;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structures of the caerins and J. Chem. Res. 139:937-961(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD11_LITGI STANDARD; PRT; 12 AA.
P62566; P56245; P81253;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Litoria gilleni (Centralian tree frog).
Litoria gilleni (Centralian tree frog).
Bukaryota, Metazoa; Chordata; Craniata; Wertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
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Pred. No. 7.3e+03;
                                                                                                          CD11 LITCH STANDARD; PRT; 12 AA. 16255; P56257; P56245; P81253; P51253; P512-UL-1998 (Rel. 36, Last sequence update) 15-UL-1998 (Rel. 36, Last annotation update) 16-Caridin 1.1/1.2/1.3. Litoria chloris (Blue-thighed frog)
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60.0%;
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           SLSFQLGLYLS 13
                             S AFKFQXGVFVA 15
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Best Local Similarity
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                                                                                                                                                                                                                                                                             -!- PTW: Isomerization alpha-beta of the Asp-4 residue in caeridin 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5 residues in caeridin 1.3.
-!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1. Amidation; Amphibian defense peptide; Direct protein sequencing.
12 12 Leucine amide.
SEQÜENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin
1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5
residues in caeridin 1.3 (By similarity)
-!- MASS SPECTROMETRY: MW=1139; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.
Aust. J. Chem. 48:1981-1987(1995).
-!- FUNCTION: Caeridins show neither neuropeptide activity nor antibiotic activity.
-!- TISSUE SPECIFICITY. Specifically secreted by the skin parotoid and/or rostral glands.
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-!- TISSUE SPECIFICITY: Specifically secreted by the skin parotoid and/or rostral glands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P62565; P56245; P81233; P812333; P812333; P812333; P812333; P812333; P812333; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amidation, Amphibian defense peptide; Direct protein sequencing
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TISSUBE-Parotoid gland;
Stone D.J.M., Maugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
Stone D.J.M., Maugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. Structures of the caerins and caeridin I from Litoria splendida.";
J. Chem. Soc. Perkin Trans. I 1:3173-3178(1992).
-:- FUNCTION: Caeridins show neither neuropeptide activity nor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 1; Length 12;
Pred. No. 7.3e+03;
0; Mismatches 4; Indels
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Pred. No. 7.38+03;
0; Mismatches 4; Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Carridin 1.1/1.2/1.3.
Litoria xanthomera (Orange-thighed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA.
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60.0%;
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60.0%;
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PRELIMINARY;
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                                                                                     Sus scrofa (Pig).
                                                                                                                    NCBI_TaxID=9823;
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                                                                          Name=collal;
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Q6LDP8
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                                                                                                     Gaps
                                                    SEQUENCE, AND MASS SPECTROMETRY.
MEDLINE=97374000; PubMed=9230483;
Steinborner S.T., Waugh R.J., Bowle J.H., Wallace J.C., Tyler M.J.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muren J.E., Naessel D.R.; "Seven tachykinin-related peptides isolated from the brain of the madeira cockroach; evidence for tissue-specific expression of
                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
50-MLY-2000 (Rel. 39, Last sequence update)
50-ULL-2004 (Rel. 44, Last annotation update)
Tachykinin-related peptide 10 (LemTRP 10).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
NCBI_TaxID=6988;
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0
                                                                                             "New caerin antibacterial peptides from the skin glands of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides 16:7-15(1997).
--- FUNCTION: Myoactive peptide. Increases the amplitude and of spontaneous contractions and tonus of hindgut muscle.
--- SUBCELDUAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Brain.
--- MASS SPECTROMETRY: MW=1436.0; METHOD=MALDI; RANGE=1-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.6%; Score 22; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 9.2e+03; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             28.6%; Score 22; DB 1; Length 12; 60.0%; Pred. No. 7.3e+03; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                         12 AA; 1141 MW; 2822551A33772728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct protein sequencing; Neuropeptide; Tachykinin. SEQUENCE 15 AA; 1438 MW; 298572F373FA7007 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 15 AA.
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Matches 6; Conserv
                                 NCBI_TaxID=79697;
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Possible insertion sequences in a mosaic genome organization upstream of the exotoxin A gene in Pseudomonas aeruginosa.";
J. Bacteriol. 172:2020-2028(1990).
EMBL, M27186; AAA26012.1;
EMBL, M27186; AAA26011.1;
NON_TER 8
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Intestine;
MEDLINE-21560060; PubMed=11704606;
Albo H.S., Inkinen K.A., Salminen U.S., Maasilta P.K., Taskinen E.I., Glumoff V., Vuorio E.I., Ikonen T.S., Harjula A.L.J.;
"Collagens I and III in a porcine bronchial model of obliterative bronchiolitis.";
Am. J. Respir. Crit. Care Med. 164:1519-1525(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
(Strain Ps318) toxA gene encoding exotoxin A, 5' end ((strain PA103)
LoxA gene encoding exotoxin A, 5' end) (Fragment)
Pseudomonas aeruginosa
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pseudomonadaceae; Pseudomonas.
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Pred. No. 9.2e+03;
2; Mismatches 2; Indels
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Pritchard A.E., Vasil M.L.;
Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TËR 1 1
SEQÜENCE 15 AA; 1680 MW; 895303298274A63A CRC64;
                                  Last sequence update)
Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence
01-JUN-2003 (TrEMBLrel. 24, Last annotatio
Type I collagen alpha 1 chain (Fragment).
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50.0%;
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Best Local Similarity 50.00,
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MEDLINE=90202723; PubMed=2156808;
Pritchard A.E., Vasil W.L.;
"Possible insertion sequences in a mosaic genome organization upstream of the exotoxin A gene in Peeudomonas aeruginosa.";
J. Bacteriol. 172:2020-2028(1990).
EMBL; M27175; AAA26011.1; -...
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Pritchard A.E., Vasil M.L.;
Pritchard A.E., Vasil M.L.;
"A mosalc genome organization upstream of the exotoxin A gene in "Peeudomonas aeruginosa: Possible insertion sequences.";
Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
EMBL; M27186; AAA26012.1; -.
NOW TER
8 AA; 1046 MW; F94371F7605721E6 CRC64;
                                                                                                                   (Fragment).
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
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                                     02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
(STRAIN PA103) TOXA GENE ENCODING EXOTOXIN A, 5' END
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA26012 PRELIMINARY; PRT; 8 AA.
AAA26012;
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
(GTRAIN PS388) TOXA GENE ENCODING EXCTOXIN A, 5' END
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  8 AA.
  PRT;
PRELIMINARY;
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Pseudomonas aeruginosa
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1 MHLIPH 6
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NCBI_TaxID=287;
AAA26011
AAA26011;
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Search completed: November 14, 2004, 13:16:24 Job time : 101 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 14, 2004, 13:03:52; Search time 18:3333 Seconds (without alignments) 78.723 Million cell updates/sec Run on:

Title: Perfect score:

US-09-831-253F-9 77 1 LDSLSPQLGLYLSPH 15 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

2523 Total number of hits satisfying chosen parameters:

l length: 0 | length: 15 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query	Length	DB	а	Description
	29	37.7	11	2	A35594	buccalin - Califor
7	24	31.2	15	~	A35417	ne
٣	24	31.2	15	4	138335	hypothetical TEL/M
4	23	29.9	11	7	PH0914	T-cell receptor be
2	23	29.9	12	7	C36201	1-aminocyclopropan
9	21	27.3	15	~	A47628	Fc gamma receptor
7	20	26.0	11	4	PC2124	aminotransferase c
æ	20	26.0	12	~	B61497	seed protein ws-17
6	20	26.0	14	~	B61597	cytochrome P450 AL
10	19	24.7	7	~	A11483	aspartate transami
11	19	24.7	10	~	A30823	bothropstoxin - ja
12	19	24.7	10	~	D60787	sperm-activating p
13	19	24.7	14	~	A28018	very late antigen-
14	19	24.7	15	7	T46625	hypothetical prote
1.5	19	24.7	15	7	PC1317	large granule L4 c
16	19	24.7	15	~	B45115	peptidylprolyl iso
17	19	24.7	15	7	C32521	hexokinase (EC 2.7
18	18.5	24.0	11	7	PT0301	Ig heavy chain CRD
19	18	23.4	9	7	JN0861	peptidyl-dipeptida
20	18	23.4	σ,	7	PC4131	hypothetical prote
21	18	23.4	10	ď	PC2044	beta-Kirilowin - M
22	18	23.4	-	~	S01749	collagen alpha 1(I
23	18	23.4	12	7	801122	photosystem II 3.7
24	18	23.4	12	0	H41946	T-cell receptor ga
25	18	23.4	7	~	B61620	locustamyotropin I
56	17	22.1		N	A37521	R-phycoerythrin ga
27	17	22.1	ω	~	T13818	cytochrome oxidase
28	17	22.1	D	7	PS0253	glycine cleavage s
53	17	22.1	10	-	ECLO3M	tachykinin III - m

placental lactogen	wound-induced proc T-cell receptor be	Ig H chain V-D-J r	porin por 1B - Ara	porin porl - Arabi	hypothetical prote	T-cell receptor be	Ig H chain V-D-J r	T-cell receptor al	glycophorin B (mis	T cell receptor al	T cell receptor al	hemoglobin alpha c	neuromedin K - pig	angiotensin I - ho
A47364	PH0771	PH1596	PA0109	PA0045	808209	A49252	PH1616	PH0782	170075	PH1758	PH1766	157650	SPPGNK	865432
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17 22.1	17 22.1	17 22.1	17 22.1	17 22.1	17 22.1	17 22.1	17 22.1	17 22.1				16 20.8		16 20.8
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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A35594
buccalin - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 09-Jul-2004
C;Accession: A35594
Ex;Cropper, B.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.Proc. Natl. Acad. Sci. US.A. 85, 6177-6181, 1988
A;Title: Structure and action of bucalin: a modulatory neuropeptide localized to an id
A;Reference number: A35594; MUID:88320404; PMID:3413086
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CRO>
A;Cross-references: UNIPROT:P20481
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Gaps ö Query Match 37.7%; Score 29; DB 2; Length 11; Best Local Similarity 60.0%; Pred. No. 56; Matches 6; Conservative 2; Mismatches 2; Indels

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1 LDSLSFQLGL 10 :|||:| 2 MDSLAFSGGL 11 g ઠ

A35417
28K scrine proteinase homolog - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004
C;Accession: A35417
R;Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.
Biochem. Biophys. Res. Commun. 170, 769-774, 1990
A;Title: Co-purification of proteases with basic fibroblast growth factor (FGF).
A;Reference number: A35417; MUD:90343797; PMID:2200404

A Status: preliminary
A Molecule type: protein
A Residues: 1-15 < HOA>
A Cross-references: UNIPROT:Q7M3G3

ö Query Match 31.2%; Score 24; DB 2; Length 15; Best Local Similarity 30.8%; Pred. No. 6.2e+02; Matches 4; Conservative 5; Mismatches 4; Indels

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Gaps

3 DSIDYRKKGYVTP 15 2 DSLSFQLGLYLSP 14 à 셤

RESULT 3 138335

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C;Species: synthetic
C;Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C;Datesion: PC2124
R;Miyazawa, K.; Kawaquchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994
A;Title: Construction of aminotransferase chimeras and analysis of their substrate special A;Reference number: JX0315; MUID:94334304; PMID:8056774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: PC2124
A;Accession: PC2124
A;Molecule type: DNA
A;Residues: 1-11 <MIX>
C;Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (EC
C;Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (EC
C;Comment: The parental enzymes catalyze the reversible amino group transfer reaction be
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A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dim
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: B61497
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A47628
R;Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Capel, P.J.A.
J. Exp. Med. 172, 19-25, 1990
A;Title: Molecular basis for a polymorphism of human Fcgamma receptor II (CD32)
A;Reference number: A47628; MUID:90293679; PMID:2141627
A;Accession: A47628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seed protein ws-17 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;bate: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: B61497
R;Hirano, H.
                                                   Gaps
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA A; Meeidues: 1-15 <mRNA C; Keywords: immunoglobulin receptor
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    Pred. No. 7.3e+02;
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50.0%; Pred. No. 2.3e+03;
tive 2; Mismatches 1;
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66.7%; Pred. No. 2.1e+03;
iive 1; Mismatches 1;
    75.0%;
                                                   6, Conservative
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                                                                                                                                  3 SLSFQLGL 10
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Best Local Similarity
Matches 6, Conserv
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C.Species: Malus domestica (apple tree)
C.Species: Malus domestica (apple tree)
C.Species: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C.Accession: C36201; C33103
R.Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990
A.Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-car A.Reference number: A36201; MUID:91045911; PMID:2122449
A.Recession: C36201
A.Recession: C3620
                                C; Species: Homo gapiens (man)
C; Species: Homo gapiens (man)
C; Species: Homo gapiens (man)
C; Accession: 13835
R; Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G. Moncogene 10, 1511-1519, 1995
A; Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusi A; Reference number: 138031; MulD:95249265; PMID:7731705
A; Accession: 138335
A; Accession: 138335
A; Accession: 138315
A; Accession: 158215
C; Comment: Translated from GB/EMBL/DDBJ
A; Residues: 1-15 < RUI>A; Residues: 1-15 < RUIA; RUIA
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C'Accession: PH0014
R'GOID, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
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C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
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hypothetical TEL/MN1 mutant fusion protein type II - human (fragment)
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A;Molecule type: mRNA
A;Residues: 1-11 <GGL>
A;Experimental source: myelin basic protein-immunized lymph node C;Keywords: T-cell receptor
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Pred. No. 6.2e+02;
0; Mismatches 1; Indels
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80.0%;
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Query Match

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Query Match

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A,Title: Fractionation of Bothrops jararacussu snake venom: partial chemical characteri: A,Reference number: A30823; MUID:89020120; PMID:3176051
A,Accession: A30823
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Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3244, 1987
A;Title: The very late antigen family of heterodimers is part of a superfamily of molec
A;Reference number: A94151; MUID:87204112; PMID:3033641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sperm-activating peptide (Ser-1, Ala-3, Gly-5 speract) - sea urchin (Hemicentrotus pulci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, Comp. Biochem. Physiol. B 89, 687-693, 1988
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentra, R;Reference number: A60787; MUID:88242184; PMID:3378407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q7M4D1
C,Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.
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C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      very late antigen-1 alpha chain - human (fragment)
N;Alternate names: VLA-1 alpha chain
C;Species: Homo sapiens (man)
C;Date: 30-Jun.1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C;Accession: A28018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Hemicentrotus pulcherrimus
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
C;Accession: D60787
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Pred. No. 3.1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14;
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A, Molecule type: protein
A, Residues: 1-14 < TAXx>
C, Keywords: duplication; heterodimer; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 2; I
Pred. No. 4.5e+03;
2; Mismatches 0;
                                                                                                                                                                                                                                         Score 19; DB 2; I
Pred. No. 3.1e+03;
1; Mismatches 0;
                                                                                                                                                                              A; Cross-references: UNIPROT: Q7L225
                                                                                                                                                                                                                                            24.7%;
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80.0%;
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60.0%;
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Matches 3; Conservative
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      Toxicon 26, 615-627, 1988
                                                                                                                      A; Molecule type: protein A; Residues: 1-10 < HOM>
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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DSMTF 11
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NyAlternate names: aspartate aminotransferase, mitochondrial
NyAlternate names: aspartate aminotransferase, mitochondrial
Cyspecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cybate: 05-Uun-1987 #sequence_revision 05-Uun-1987 #text_change 20-Aug-1999
CyAccession: Al1483 #sequences of the coenzyme-binding peptide in the cytoplasmic and the mitoch A;Reference number: Al1483; MUID:76039441; PMID:1180894
A;Reference number: Al1483; MUID:76039441; PMID:1180894
A;Residues: 1-7 cAM>
A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A30823

Ochropstoxin - jararacussu (fragment)

C;Species: Bothrops jararacussu (jararacussu)

C;Species: Bothrops jararacussu (jararacussu)

C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004

C;Accession: A30823

R;Homsi-Brandeburgo, M.I.; Queiroz, L.S.; Santo-Neto, H.; Rodrigues-Simioni, L.; Giglio,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Rattus norvegicus (Norway rat)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                Gaps
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                                                                                                                                                  Length 12;
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                                                                                                                                                  Score 20; DB 2; I
Pred. No. 2.5e+03;
3; Mismatches 4;
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A;Molecule type: protein
A;Residues: 1.12 <HIR>
A;Cross-references: UNIPROT:Q7M1H9
C;Keywords: seed
                                                                                                                                                  26.0%;
30.0%;
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Best Local Similarity 30.0
Matches 3; Conservative
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1 DTISFNFNQF 10
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Best Local Similarity
Matches 5; Conserv
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4 MGLY 7
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C;Accession: T46625
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
Submitted the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is dc
A;Reference number: 223105
A;Reference number: 223105
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-15 CGHA
A;Residues: 1-15 CGHA
A;Experimental source: strain s6PT2xs6FP3; 8 month seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Targe granule L4 chain - horseshoe crab (Tachypleus tridentatus) (fragment)
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: PC1317
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J; Biochem. 114, 307-316, 1993
A;Reference number: PC1309; MUID:94110249; PMID:8282718
A;Accession: PC1317
A;Accession: PC1317
A;Molecule type: protein
A;Residues: 1-15 <SHI>
C;Comment: This protein participates in immobilization of invading microbes.
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ö Query Match

24.7%; Score 19; DB 2; Length 15;
Best Local Similarity 38.5%; Pred. No. 4.8e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 2 DSLSFQLGLYLSP 14 ઠે

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Gарв

Search completed: November 14, 2004, 13:17:23 Job time : 18.3333 secs

3 DEIIFHLLXKASP 15

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RESULT 1
FRE1_LITIN STANDARD; PRT; 12 AA.

ID FRE2_LITIN STANDARD; PRT; 12 AA.

AC PS2021;

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                Q97233
Q39633
Q63469
Q53469
Q9TWQ6
Q82520
SODM_RANCA
CD11_LITCH
CD11_LITGI
CD11_LITGI
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70.0%;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
   0 - 0 0 0 0 0 0 - - - -
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Matches 7; Conservative
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Bacteriophage Kul.
 1 LDSLSFQLGL 10
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LDALSGILGL 12
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Frenatin 1
SEQUENCE
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038573
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091cx8 tt virus. 0
091cx8 tt virus. 0
091cx7 tt virus. 0
09pru8 gallus gall
09uvw brachydanio
09sc61 picea abies
09r4t0 rhodbacter
09sc61 picea abies
09sc51 picea abies
09sc52 erwinia any
Cag27500 erwinia a
Cag2752 erwinia a
Cag2752 erwinia a
Cag2752 erwinia a
Cag2752 erwinia a
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Cag2760                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P82021 litoria inf
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                                                                                                             November 14, 2004, 11:57:26; Search time 40.0532 Seconds (without alignments) 215.479 Million cell updates/sec
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                5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          1825181 segs, 575374646 residues
              GenCore version (c) 1993 - 2004
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Q91CX8
ASP1_LACSN
Q91CX7
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Q7LZ16
CAA40176
UCRQ_EQUAR
Q9TR41
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Q38573
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Maximum Match 100%
Listing first 45 summaries
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Q9ZYV9
Q6RJY6
AAR83863
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CAG27598
CAG27600
CAG27725
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Q8UVW4
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Q9R4T0
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Q9ZYX8
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P92072
O9TR52
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Gapop 10.0 , Gapext 0.5
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1: uniprot sprot:*
2: uniprot_trembl:*
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                                                                                protein search, using
                                                                                                                                                                             US-09-831-253F-9
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Match Length DB
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Perfect score:
Sequence:
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Maximum DB
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litoria spl
litoria xan
                                     cucumis sat
mycobacteri
tachypleus
                     plasmodium
nicotiana s
                                                            influenza a
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                                                                             litoria
                            091213
039633
039633
0091469
0082520
082520
082567
062566
062566
062565
               Q9zaa0
Q7rde9
Q9R1W6
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SEQUENCE, AND MASS SPECTROMETRY.

TISSUB-Skin secretion;

MEDLINE=97366637; PubMed=9225251;

Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;

Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;

"The structures of the frenatin peptides from the skin secretion of the giant tree frog Litoria infrafrenata.";

J. Pept. Sci. 2:117-124(1996).

-!- FUNCTION: Wide spectrum antimicrobial peptide.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
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-!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.
Amidation; Amphibian defense peptide; Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
Levivirus.
Litoria infrafrenata (Giant tree frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Bukaryota, Batracchia, Anura, Neobatrachia, Hyloidea, Hylidae,

Pelodryadinae, Litoria.
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Pred. No. 8.9e+02;
1; Mismatches 2; Indels
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C622550BC365B72D CRC64;
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Last annotation update)
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50.0%;
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Matches 5, Conservative
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7 LKTQAGVHLNP 17
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1 SFKKGLFL 8
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Name=ORF1;
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P82648;
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ASP1_LACSN
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MEDLINE=96207403; PubMed=8615017; Groeneveld H., Oudot F., van Duin J.V.; "RNA phage Holder F., van Duin J.V.; "RNA phage Holden an insertion of 18 nucleotides in the start codon of its lysis gene."; Virology 218:141-147(1996). EMBL. $8178; ADIA1371.1; -.. EMBL. $60; GO:0019028; C:viral capsid; IEA. GO: GO: 0005198; F:structural molecule activity; IEA.
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Virology 288:358-368 (2001).
EMBL; AB060623; BA869943.1; -.
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BEDLINE=21488921; PubMed=11601907;
Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
Yoshikawa A.;
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MEDLINE=21488921; Pubmed=11601907;
Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
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Viruses; ssDNA viruses; Circoviridae; Anellovirus.
NCBI_TaxID=68887;
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TT Virus:
Viruses; ssDNA viruses; Circoviridae; Anellovirus
NCBI_TaxID=68887;
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18 AA; 1825 MW;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Q91CX8;
01-DEC-2001 (TEMBLE-1 19,
01-DEC-2001 (TEMBLE-1 19,
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  "Heterogeneous distribution of TT virus of distinct genotypes multiple tissues from infected humans."; Virology 288:358-368(2001).
EMBL, AB060615; BAB69936.1; -.
   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 44, Last annotation update)
Acid shock protein 1 (Fragment)
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco)
Bacteria, Firmicutes; Lactobacillales; Lactobacillus
NCBL_TAXID=1625;
   SEQUENCE FROM N.A.
MEDLINE-21488921; PubMed=11601907;
Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
Yoshikawa A.;
   Length 23;
  Score 26; DB 1; Length 15; Pred. No. 1.7e+03;
  Length 16;
Virology 288:358-368(2001). EMBL, AB060605; BAB6928.1; -. NON TER SEQÜÜENCE 23 AA, 2710 MW; 51246068099E107F CRC64;
   E152327E7C679238 CRC64;
   575853B4DFB030A8 CRC64;
  Last sequence update)
Last annotation update)
   TT virus.
Viruses; ssDNA viruses; Circoviridae; Anellovirus.
NCBI_TaxID=68887;
   Score 27; DB 2; I
Pred. No. 1.8e+03;
  Score 26; DB 2;
Pred. No. 1.8e+03;
  3; Mismatches
  2; Mismatches
  Created)
  PRT;
  33.8%;
62.5%;
   SEQUENCE 15 AA; 1509 MW;
   h 35.1%;
Similarity 45.5%;
5; Conservative
   16 AA; 1793 MW;
  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
AMPA receptor subunit 2 (Fragment).
Name=gria2-1; Synonyms=glur2a;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TAXID=7955;
  SEQUENCE FROM N.A.
MEDLINE=21617183; PubMed=11741603;
MEDLINE=2.1617183; PubMed=11741603;
Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.;
Kung S.-S., Chen Y.-C., Len APPA receptor subunit 2 (GRIA2) transcript
evolves no later than the appearance of cartilaginous fishes.";
FEBS Lett. 509:277-281(2001).
  Picea ables (Norway spruce) (Picea excelsa).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
VCBI_TaxID=3329;
   SEQUENCE FROM N.A.
MEDLINE=20040041; PubMed=10571856;
Pearce S.R., Stuart-Rogers C.M., Knox M.R., Kumar A., Ellis N.T.,
  Flavel A.J.;
"Rapid isolation of plant Tyl-copia group retrotransposon LTR sequences for molecular marker studies.";
Plant J. 19:711-717(1999).
EMBL; AJ243314; CAB65328.1; -.
   Score 26; DB 2; Length 19; Pred. No. 2.2e+03; 3; Mismatches 3; Indels
  33.8%; Score 26; DB 2; Length 23; 50.0%; Pred. No. 2.7e+03; tive 2; Mismatches 2; Indels
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19 19 19
19 AA; 2101 MW; 19490444CB82EF5B CRC64;
   23 AA; 2678 MW; 6C9FD7957DCFAB64 CRC64;
   Last sequence update)
Last annotation update)
                                    19 AA.
  23 AA
   EMBL, AF350048; AAL51190.1; -. ZFIN; ZDB-GENE-020125-3; gria2.1. GO; GO:0004872; F:receptor activity; IEA.
  Created)
  PRT;
   33.8%;
   01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, Ribonuclease H (Fragment).
   45.5%;
  Local Similarity 50.0
  Local Similarity 45.
                                    PRELIMINARY;
  PRELIMINARY;
  2 DSLSFQLGLYL 12
  4 LSFQLGLY 11
   16 IQFMLGVY 23
   23
   Name=rnaseH;
  Receptor.
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   Matches
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  Kita E., Mateni N., Sawaki M., Mikasa K., Katsui N.;
"Murine tumorlytic factor, immunologically distinct from tumor
necrosis factor-alpha and -beta, induced in the serum of mice treated
with a T-cell mitogen of Corymbacterium kutscheri.";
Immunol. Lett. 46:101-106 (1995).
SEQUENCE 18 AA; 2049 MW; 3544227DA4EFD1D0 CRC64;
  Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
  Gaps
 Gaps
  NEDLINE=95105151; PubMed=7806494;
Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J., Yazaki Y., Hirai H.;
Yazaki Y., Hirai H.;
"Characterization, partial purification, and peptide sequencing of pl30,the main phosphoprotein associated with v-Crk oncoprotein.";
J. Biol. Chem. 269:32740-32746(1994).
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   01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
1130-PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO
  Length 17;
  Score 26; DB 2; Length 18;
Pred. No. 2.1e+03;
2; Mismatches 2; Indels
   1; Indels
  2; Indels
   17 17
17 AA; 1861 MW; 379058CDE44F8879 CRC64;
   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
TUMORLYTIC factor (Fragment).
  Query Match 33.8%; Score 26; DB 2; Best Local Similarity 62.5%; Pred. No. 2e+03; Matches 5; Conservative 1; Mismatches 5
  17 AA.
   18 AA.
 Mismatches
  PRT;
  SEQUENCE.
MEDLINE=96078161; Pubmed=7590903;
 3;
  33.8%;
  4; Conservative
4; Conservative
  PRELIMINARY;
   PRELIMINARY;
   8 LGLYLSPH 15
                              QLGLYLSP 14
  3 QAGLHINP 10
   7 QLGLYLSP 14
   MGLYMLTH 15
  2 OOGLYQAP 9
  Query Match
Best Local Similarity
Matches 4; Conserv
   NCBI_TaxID=9031;
   NON TER
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SEQUENCE
   (Fragment)
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32.5%;
66.7%;
  32.5%;
   SEQUENCE 22 AA; 2245 MW;
  6; Conservative
  Local Similarity 66.7
nes 6, Conservative
  PRELIMINARY;
   PRELIMINARY;
  5 SFQLGLYLS 13
  11 SSSLGLYQS 19
  13
   13
  Local Similarity
  5 SFQLGLYLS
   Harpin (Fragment).
HRPW.
   Erwinia amylovora.
     Erwinia amylovora
   SEQUENCE FROM N.A
   Harpin (Fragment
   NCBI_TaxID=552;
   CAG27600;
   CAG27725;
  CAG27600
  Query Match
  Query Match
   CAG27725
  RESULT 14
CAG27600
  Matches
  Matches
   RESULT 15
   CAG27725
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   TX OCC BE DIT OCC SOC 
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   SEQUENCE.
MEDLINE-95160605; PubMed-7857198;
Sabaty M., Gagnon J., Vermeglio A.;
Induction by nitrate of cytoplasmic and periplasmic proteins in the photodenitrifier Rhodobacter sphaeroides forma sp. denitrificans under anaerobic or aerobic condition.";
Arch. Microbiol. 162:335-343(1994).
  Gaps
   Gaps
   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Erwinia.
NCBI_TaxID=552;
   Q98410;

Q1-MAY-2000 (TERMELrel. 13, Created)

01-MAY-2000 (TERMELrel. 13, Last sequence update)

01-MAY-2000 (TERMELrel. 17, Last annotation update)

Periplasmic protein 5 (Fragment).

Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteraceae;

Rhodobacteraceae; Rhodobacter.
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   ö
  Score 25; DB 2; Length 15;
Pred. No. 2.6e+03;
2; Mismatches 2; Indels
  Score 25; DB 2; Length 22;
Pred. No. 3.9e+03;
0; Mismatches 3; Indels
  SEQUENCE FROM N.A.

STRAIN-NCPPB 2293, PD 2915, and NCPPB 2292;
GIOSTIAN SCOTTICHINI M.;
Submitted (AFR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ698835; CAG27600.1;
EMBL; AJ698834; CAG27785.1;
EMBL; AJ698834; CAG27785.1;
NON_TER
  CC34D82FCC1BC69B CRC64;
   Last sequence update)
Last annotation update)
   Last sequence update)
Last annotation update)
   15 AA
   22 AA
   22 AA.
   Created)
   Created)
   PRT;
   PRT;
   CAG27598 PRELIMINARY;
CAG27599;
10-MAY-2004 (TERMELrel. 27, La
10-MAY-2004 (TERMELrel. 27, La
10-MAY-2004 (TERMELrel. 27, La
Harpin (Fragment).
  32.5%;
66.7%;
  Query Match
32.5%;
Best Local Similarity 55.6%;
Matches 5; Conservative
   05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
Harpin (Fragment).
  22 AA; 2245 MW;
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   6; Conservative
  2 DSLSFQLGL 10
  4 DSETFQSGM 12
   5 SFQLGLYLS 13
   11 SSSLGLYOS 19
  Query Match
Best Local Similarity
Matches 6; Conserv
   Erwinia amylovora.
   Name=hrpW;
  SEQUENCE
   O6ZXI6;
   9IXZ90
                                     Q9R4T0
   RESULT 12
Q6ZXI6
RESULT 11
Q9R4T0
   CAG27598
ID CAG2
AC CAG2
DT 10-M
DT 10-M
DT 10-M
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SEQUENCE FROM N.A.

STRAIN-NCPPB 2293;
Giorgi S., Scortichini M.;
Molecular characterization of Erwinia amylovora strains isolated from different host plants through genomic fingerprinting and RFLP analysis and sequencing of hrpw and dspA genes.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2004) to the EMBL/GenBank/DDBJ CATABASES.

SNDMITER 22
22
NOW TER 22
22
SEQUENCE 22 AA; 2245 MW; CC34DB2FCCIBC69B CRC64;
   STRAIN=NCPBB 2292;
Giorgi S., Scortichini M.;
Submitted (ARR-2004) to the EMBL/GenBank/DDBJ databases.
CAG27598.1;
NON_TER 22.
   Gaps
   Gaps
   Erwinia amylovora.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Erwinia.
NCBL_TaxID=552;
[1]
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Erwinia.
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Enterobacteriaceae; Erwinia.
NCBI_TaxID=552;
   ;
0
   .
0
  Score 25; DB 2; Length 22; Pred. No. 3.9e+03; 0; Mismatches 3; Indels
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Pred. No. 3.9e+03;
0; Mismatches 3; Indels
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  10-WAY-2004 (TrEMBLrel. 27, Created)
10-WAY-2004 (TrEMBLrel. 27, Last sequence update)
10-WAY-2004 (TrEMBLrel. 27, Last annotation update)
  10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
  22 AA
   22 AA
   PRT;
```

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RP SEQUENCE FROM N.A.

RC STRAIN=PD 2915;
RA Glorgia S., Scortichini M.;
RT different host plants through genomic fingerprinting and RFLP analysis
RT and sequencing of hrpN and dspA genes.";
RT and
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November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds (without alignments) 155.938 Million cell updates/sec
5.1.6
Çompugen Ltd.
   Total number of hits satisfying chosen parameters:
   283416 segs, 96216763 residues
GenCore version
Copyright (c) 1993 - 2004
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
  1 LDSLSFQLGLYLSPH 15
  US-09-831-253F-9
  PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
  Minimum DB seq length: 0 Maximum DB seq length: 23
  Title:
Perfect score:
Sequence:
   Scoring table:
  OM protein
   Database :
   Searched:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OLGLYL 12 OLGLYL

RESULT 2

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hypothetical prote buccalin - Califor high conductance c Ig H chain V-D-J r Ig H chain V-D-J r 28K serine protein hypothetical TEL/M hypothetical prote pyrrologuinoline q Fc gamma receptor thrombospondin pre anti-angiotenain, insulin-like growt 1-aminocyclopropan myosin light chain formylmethanofuran small granule S2 c amylase (EC 3.2.1. gene hMLH1 protein matrix protein M1 ribosomal protein DNA-directed RNA p pyrroloquinoline q aminotransferase c seed protein ws-17 I-cell receptor be photosystem I 8.0K I-cell receptor al probable catalase Description S10876 A35594 B53145 PH1634 A35417 138335 \$29326 \$40914 \$42411 \$58946 \$6000 \$83397 PC1309 A39729 I52721 S20453 A47628 S55501 T10123 Query Match Length DB Score Result No.

| proteasome chain 6 phospholipase A2 ( kinase-related tra chymotrypsin I (EC T-cell receptor al hypothetical 2.5K carboxylesterase ( hypothetical prote aspartate transami bothropstoxin - ja sperm-activating p very late antigen- hypothetical prote large granule L4 c peptidylprolyl iso hexokinase (EC 2.7 | RESULT 1 S.10876  Mypotherical protein - human C.5Species Hear Homo sapiens (man) C.5Species 104-Dec-1992 #text_change 18-Nov-1994 C.5Accession: S10876 C.5A |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| \$09087<br>PS0332<br>PS0332<br>A56900<br>\$03505<br>\$03505<br>A145268<br>A1483<br>A1483<br>A1483<br>A1483<br>A1662<br>PC1317<br>B45115<br>C32521                                                                                                                                                              | ALIGNMENTS rision 04-Dec-1 3, D.M.; Pletu, 3, 1159-1166, 4111ebrand fact, 4111ebrand fact, 88268889; PMID Score 30; DB Score 30; DB Core 30; DB Score 30; DB                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 0000000000000000                                                                                                                                                                                                                                                                                               | _red<br>On 1:<br>Wn UID 558                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 18<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20                                                                                                                                                                                                                               | ein - human<br>apiens (man)<br>92 #sequence_rev<br>76<br>Kerbiriou-Nabias<br>Res. Commun. 15<br>n gene for von W<br>r: \$10876; MUID:<br>76<br>tion not shown<br>DNA<br>cass<br>s: EMBL:X07258<br>s: EMBL:X07258                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                          | protein - mon sapine sec-1992 #sec 510876  |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                         | cal process the process of the proce |
| 0 H G W W W W W W W W W W W W W W W W W W                                                                                                                                                                                                                                                                      | RESULT 1 S.10876 S.10876 S.10876 S.10876 S.20876 S.208 |

Duccalin - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Date: 14-Sep-1990 #sequence\_revision 14-Sep-1990 #text\_change 09-Jul-2004
C;Accession: A35594
R;Cropper, B.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.
Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988
A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an id
A;Reference number: A35594; MUID:88320404; PMID:3413086
A;Accession: A35594
A;Molecule type: protein
A;Residues: 1-11 <CRO>
A;Cross-references: UNIPROT:P20481

Gaps ö DB 2; Length 11; 2; Indels Query Match 37.7%; Score 29; DB Best Local Similarity 60.0%; Pred. No. 56; Matches 6; Conservative 2; Mismatches

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\*|||:| || MDSLAFSGGL 11 셤

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RESULT :

1 LDSLSFQLGL 10

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C; Species: Homo sapiens (man)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C; Accession: 138335
R; Buljs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G
Oncogene 10, 1511-1519, 1995
Oncogene 10, 1511-1519, 1995
A; Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fus)
A; Reference number: 138335
A; Accession: 138335
  A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-15 < 2017.
A; Residues: 1-15 < 2017.
A; Cross-references: EMBL:X85024; NID:g971471; PIDN:CAAS9397.1; PID:g971472
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   hypothetical TEL/MN1 mutant fusion protein type II - human (fragment)
  4; Conservative
   Conservative
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A,Map position: 22q11/12p13
C,Keywords: fusion protein
  | : |:||
SIECGIYL 16
  S SPOLGLYL 12
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Best Local Similarity
Matches 4; Conserv
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   11 YLSPH 15
  2 YRSPH 6
  A; Accession: T07427
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  Genetics:
  RESULT 8
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high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment) C, Species: Bos primigenius taurus (cattle)
C, Species: Bos primigenius taurus (cattle)
C, Species: Bos primigenius taurus (cattle)
C, Accession: B53145
R, Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
A, Title: Subunit composition of the high conductance calcium-activated potassium channel A, Reference number: A53145; MUID: 94140798; PMID: 7508434
A, Accession: B53145
A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-19 < KNA>
A, Residues: 1-10 <
   immunodeficiency in B-less mice
   C,Accession: A35417
R;Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.
Biochem. Biophys. Res. Commun. 170, 769-774, 1990
A;Title: Co-purification of proteases with basic fibroblast growth factor (FGF).
A;Reference number: A35417; MUID:90343797; PMID:2200404
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   "Ig H chain V-D-J region (clone B-less 213) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Dinn-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1634
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Reference number: PH1634
A;Reference pH1634
A;Residues: 1-16 <-LEV-
A;Residues: 1-16 <-LEV-
A;Respecimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
  28K serine proteinase homolog - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C;Accession: A35417
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0
   31.2%; Score 24; DB 2; Length 15; ilarity 30.8%; Pred. No. 6.2e+02; Conservative 5; Mismatches 4; Indels
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35.1%; Score 27; DB 2; Length 19;
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  32.5%;
80.0%;
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   VEFYQGSVLNPH 16
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A;Residues: 1-15 <HOA>
   Best Local Similarity
Matches 4; Conserv
  Query Match
Best Local Similarity
Matches 4; Conserv
   11 YLSPH 15
  6 YYSPH 10
   Query Match
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hypothetical protein 22, psbA 5'-region - Japanese black pine chloroplast C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C; Accession: 329326; T07437, T074
  A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-22 < TSUS
A;Cross-references: UNIPROT:Q37112; EMBL:D11467; NID:g344007; PIDN:BAA02023.1; PID:g3440
B;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
R;Wakasugi, T.; Sugiura, M.
A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genom.
A;Reference number: 216030; MUID:95024047; PMID:7937893
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   A;Cross-references: EMBL:D17510; NID:g529643; PIDN:BAA04307.1; PID:g1262588
  Gaps
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  T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C,Species: Rattus norvegicus (Norway rat)
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Score 24; DB 4; Length 15;
Pred. No. 6.2e+02;
0; Mismatches 1; Indels
   Length 22;
  Indels
  31.2%; Score 24; DB 2; Le 50.0%; Pred. No. 9.3e+02; iive 2; Mismatches 2;
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       31.2%;
80.0%;
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formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium N.Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentifica C;Species: Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Accession: A58946 [A.Accession: A58946] [A.Accession: A58946] [A.Accession: A58946] [A.Accession: A58946] [A.Accession: A78946] [A.Accession: A78946] [A.Accession: A78946] [A.Accession: A78946] [A.Accession: A58946] [A.Accession: A58
   A; Molecule type: protein
A; Mesidues: 1-17 + CHOC.
A; Note: the authors identify this peptide as the amino terminus of chain B, but it appe C; Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreduct
  C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A31397
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim ..., Lory, S.; Olson, M.V.
  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path. A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83397
  photosystem I 8.0K G chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0690
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaH and psaL are A;Reference number: PQ0667; MUID:94105345; PMID:8278548
  A,Cross-references: UNIPROT:Q9ZAAO, GB:AE004625, GB:AE004091, NID:g9947983, PIDN:AAG053
A,Experimental source: strain PAO1
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   Gaps
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   A,Molecule type: protein
A,Residues: 1-23 AOBO>
C,Superfamily: 2h Aobosstem I chain V
C,Superfamily: chloroplast; photosynthesis; photosystem I; thylakoid
   Score 23; DB 2; Length 17;
Pred. No. 1.1e+03;
1; Mismatches 0; Indels
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Pred. No. 1.5e+03;
1; Mismatches 3;
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   29.9%;
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  Best Local Similarity
Matches 4; Conserv
  6 FOLGL 10
  10 FOIGL 14
   A; Status: preliminary A; Molecule type: DNA A; Residues: 1-23 <STO>
    13 LSPH 16
   Query Match
   PQ0690
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   à
                              C; Accession: PH0914

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, L.D.
J. Exp. Med. 174, 1467-1476, 1991
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergia A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Recession: PH08914
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized lymph node
C;Keywords: T-cell receptor
   C;Accession: C36201, C33103

R;Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 7391-7934, 1999

A;Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-car

A;Reference number: A36201; MUID:91045911; PMID:2122449

A;Accession: C36201

A;Accession: C36201

A;Moslecule type: Protein

A;Residues: 1-12 <YIP-

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A;Cross-references: UNIPROT:Q9FUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:O24062

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A;Cross-references: UNIPROT:Q9FUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q4062

A;Cross-references: UNIPROT:Q9FUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q4062

A;Cross-references: Carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph

F;4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
   myosin light chain kinase - chicken

C;Species: Gallus gallus (chicken)

C;Species: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A42411

R;Leachman, S.A.; Gallagher, P.J.; Herring, B.P.; McPhaul, M.J.; Stull, J.T.

J. Biol. Chem. 267, 4930-4938, 1992

A;Title: Biochemical properties of chimeric skeletal and smooth muscle myosin light chain

A;Reference number: A42411; MUID:92165861; PMID:1371510
   1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment) C;Species: Malus domestica (apple tree)
  ö
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C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
   C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
  Gaps
   Gaps
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   Status: preliminary, not compared with conceptual translation; Molecule type: nucleic acid; protein
   Length 12;
   Length 16;
   Score 23; DB 2; Length 11; Pred. No. 6.7e+02; 1 Mismatches 0; Indels
   Score 23; DB 2; Length 12;
Pred. No. 7.3e+02;
0; Mismatches 2; Indels
  Query Match 29.9%; Score 23; DB 2; Length 16; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 4; Conservative 0; Mismatches 0; Indels
   A;Cross-references: UNIPROT:Q7LZ16
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:84332)
   29.9%;
   29.9%;
  Query Match
Best Local Similarity 66.7
Matches 4; Conservative
   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
   3 SLSFOLGL 10
  SLSKDLGL 8
  ||||::
DSLSYE 10
  2 DSLSFQ 7
   A; Residues: 1-16 < LEA>
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C; Genetics:

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A, Gene: pqqA; PA1985

```
probable catalase (EC 1.11.1.6) - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Species: Cucumis sativus (cucumber)
C;Species: hcJul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10123
R;Toyama, T.; Teramoto, H.; Takeba, G.; Tsuji, H.
R;Reference number: Z16946; MUID:96104306; PMID:8564304
A;Reference number: Z16946; MUID:9610306; PMID:96109475; PIDN:BAA09701.1; PID:9119
A;Reperimental source: seedling; cotyledons
C;Keywords: oxidoreductase
  C; Accession: PC1309
R; Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J. Blochem. 114, 307-316, 1993
A; Reference number: PC1309; MUID: 94110249; PMID: 8282718
A; Accession: PC1309
A; Cross-references: UNIPROT: O9TWQ6
C; Comment: This protein contributes to a self-defense system against invaders.
  ö
   ä
  ö
  small granule S2 chain - horseshoe crab (Tachypleus tridentatus) (fragment) C;Species: Tachypleus tridentatus C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
  Gaps
  Gaps
   Gaps
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   1;
   Ouery Match 29.2%; Score 22.5; DB 2; Length 19; Best Local Similarity 54.5%; Pred. No. 1.5e+03; Matches 6; Conservative 2; Mismatches 2; Indels
29.9%; Score 23; DB 2; Length 23; 40.0%; Pred. No. 1.5e+03; tive 3; Mismatches 3; Indels
   Query Match 29.9%; Score 23; DB 2; Length 23; Best Local Similarity 50.0%; Pred. No. 1.5e+03; Matches 4; Conservative 2; Mismatches 2; Indels
  Search completed: November 14, 2004, 12:03:15
Job time : 10.2553 secs
                               Best Local Similarity 40.0
Matches 4; Conservative
  4 LSFOLGLYLSP 14
  |:|: | | ||
2 LAFRXGRY-SP 11
  4 LSFQLGLYLS 13
   | |:: || :
12 LGFEVTLYFA 21
   : | |: ||
9 VGQKLAPH 16
   8 LGLYLSPH 15
Query Match
  RESULT 15
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Human sec Novel hum Human sec Human sec

ALIGNMENTS

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AAY93106 standard; peptide; 15

HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst HCV nonst protea V nonst V nonst V nonst V nonst V nonst

Abro0714 Abr00725 Abr00725 Abr00725 Abr00726 Aar91038 Abr00732 Abr00733 Abr00735 Abr00741 Abr00742 Abr00742 Abr00742 Abr00742 Abr00742 Abr00743 Abr00744 Abr00744 Abr00744 Abr00743 Abr00744 Abr00744 Abr00744 Abr00744 Abr00744 Abr00744 Abr00743 Abr00744 Abr00744 Abr00744 Abr00744 Abr00744 Abr00744 Abr00743 Abr00744 Abr

ABRO0714
ABRO0725
ARR00725
ARR01038
ARR00732
ABR00733
ABR00733
ABR00734
ABR00735
ABR00741
ABR00741
ABR00741
ABR00742
ABR00742
ABR00745
ABR00745
ABR00745
ABR00745
ABR00745
ABR00745
ABR00746
ABR

```
RESULT 1
  AAY93106
   THE SECTION OF SECTION
   Aay91106 Transform
Aay92953 Transform
Adm29169 Hepatitis
Aab66433 Peptide d
Aar82557 Beyine PL
Aag83462 Arabidops
Abp58975 Human I k
  Miniature
G protein
Rabbit 3-
  ; Search time 43.4043 Seconds (without alignments)
123.973 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Description
  Adv. 2253 Adm. 22953 Adm. 22959 Adm. 229169 Adm. 229169 Adm. 229169 Adm. 229176 Adm. 22917
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
   2002273 seqs, 358729299 residues
  SUMMARIES
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   November 14, 2004, 11:57:25
   OM protein - protein search, using sw model
  AAG83462
ABP58975
AAM47809
ABP82548
  AAW71733
AAE09350
AAE10097
ABU97358
ABO12018
ADE29276
ABP46134
   AAY93106
AAY92953
ADM29169
AAB68433
AAR82557
   BLOSUM62
Gapop 10.0 , Gapext 0.5
  geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003bs:*
   1 LDSLSFQLGLYLSPH 15
  A_Geneseq_23Sep04:*
.: geneseqp1980s:*
: geneseqp1990s:*
   US-09-831-253F-9
77
   B
   Query
Match Length
                             Copyright
  seq length: 0
seq length: 23
  Title:
Perfect score:
   Scoring table:
   Score
  Minimum DB
Maximum DB
   ••
  Searched:
   Sequence:
  Database
   Run on:
   Result
No.
  22221098765
222210987654321098765
```

Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.

99WO-ES000375 98ES-00002465

23-NOV-1999; 24-NOV-1998;

02-JUN-2000

WO200031135-A1

Homo sapiens

Transforming growth factor inhibitory peptide P152.

(first entry)

08-NOV-2000

AAY93106;

|   | PA     | (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.                            |
|---|--------|---------------------------------------------------------------------------|
|   | X      |                                                                           |
|   | PI     | Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;            |
|   | PI     | Borras Cuesta F;                                                          |
|   | X      |                                                                           |
|   | DR     | WPI; 2000-411935/35.                                                      |
|   | XX     |                                                                           |
|   | PT     | Peptides that antagonize binding of transforming growth factor betal,     |
|   | PT     | useful for treatment of liver disease, especially cirrhosis, are partial  |
|   | PŢ     | sequences of the factor or its receptors.                                 |
|   | X      | ,                                                                         |
|   | PS     | Disclosure, Page 33; 86pp; Spanish.                                       |
|   | XX     |                                                                           |
|   | ႘      | The invention relates to synthetic peptides that antagonise the binding   |
|   | ႘      | of transforming growth (TGF) factor betal (TGF-b1) to its receptor in     |
|   | ႘      | vivo which have partial amino acid sequences identical, or similar, with  |
|   | ე<br>ე | those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  |
|   | ႘      | examples of the peptides of the invention. The peptides act by            |
|   | ე      | competitive inhibition of the binding of TGF-b1 to its receptors, e.g.    |
|   | ႘      | they are inhibitors of stimulation of collagen synthesis in liver cells   |
|   | ဗ      | and inhibitors of synthesis of proteolytic enzymes able to degrade the    |
| _ | ႘      | extracellular matrix. The peptides, their mimetopes and/or DNA (or        |
|   | ပ္ပ    | expression systems) encoding the peptides are used for treatment of liver |
| _ | ႘      | disease, specifically cirrhosis                                           |

Human ion Human ion Amino aci Human zin Novel hum Human BLy scFv VHCD

Human pep HCV nonst HCV nonst HCV nonst

Exemplary

ADG96961 ADN03302 AAB07274

ABR00682 **ABR00699** ABR00693

Human pep HCV nonst HCV nonst

AAM97619 ABR00703 ABR00706

Best Loc Matches

RESULT 2

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AAY9295

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The present invention describes a DNA vaccine which comprises a plasmid containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV). Also described: (I) a recombinant adenovirus vaccine including an adenovirus containing 2-6 kb of total antigen gene of HCV; (2) a vaccine including an infection. The DNA vaccine has virucide activity. The DNA vaccine is useful in treating or preventing HCV infection. The pNA vaccine is useful in treating or preventing HCV infection. The present sequence represents a peptide from the HCV peptide pool used for the investigation of cellular immune response in the exemplification of the present
  New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen gene of hepatitis C virus'(HCV), useful in treating or preventing HCV
   DNA vaccine, vaccine, antigen gene, antigen, hepatitis C virus, HCV, recombinant adenovirus vaccine, adenovirus, HCV infection, hepatitis C virus infection; infection, virucide.
  Hepatitis C virus cellular immune response related peptide.
   Peptide derived from human G-protein coupled receptor HG67.
  Lee CG;
  Score 33; DB E
Pred. No. 90;
2; Mismatches
  Disclosure; Fig 20e; 165pp; English.
  Park S,
                Ą.
  AAB68433 standard; peptide; 16 AA.
                ADM29169 standard; peptide; 20
   27-SEP-2002; 2002KR-00058712, 06-NOV-2002; 2002KR-00068496,
  42.9%;
66.7%;
  24-SEP-2003; 2003WO-KR001951
  POSTECH FOUND.
DONG-A PHARM CO LTD.
DAEWOONG CO LTD.
  Yang S,
  23-JUL-2001 (first entry)
  (first entry)
   Conservative
  10
  | :|||:||
11 DEVSFQVGL 19
  (GENE-) GENEXINE INC.
   WPI; 2004-305120/28.
  Local Similarity
es 6; Conserv
   DSLSFQLGL
  Sung YC, Youn J,
   Hepatitis C virus.
  WO2004028563-A1.
   Sequence 20 AA;
   (POSC-) POSCO
  01-JUL-2004
   08-APR-2004.
  invention.
   Synthetic
   infection
   AAB68433;
   ADM29169;
  ~
  Query Match
  (POST-)
(DONG-)
   (DAEW-)
  AAB68433
ID AAB6
XX
AC AAB6
XX
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DT 23-C
4DM29169
  RESULT
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  The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides ANY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
  Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
   Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
  Gaps
  Gaps
   Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
  ö
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   Score 77; DB 3; Length 15;
Pred. No. 5e-07;
Mismatches 0; Indels
   100.0%; Score 77; DB 3; Length 15; ilarity 100.0%; Pred. No. 5e-07; Conservative 0; Mismatches 0; Indels
  Transforming growth factor inhibitory peptide #9.
  (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
   AAY92953 standard; peptide; 15 AA
   Claim 10; Page 82; 86pp; Spanish.
  .
  100.0%;
   99WO-ES000375
  98ES-00002465
  1 LDSLSFQLGLYLSPH 15
   1 LDSLSFOLGLYLSPH 15
   1 LDSLSFQLGLYLSPH 15
  1 LDSLSFOLGLYLSPH 15
   (first entry)
   Query Match
Best Local Similarity 100.
Matches 15; Conservative
  WPI; 2000-411935/35.
   Local Similarity
les 15; Conser
  Borras Cuesta F;
   Sequence 15 AA;
   WO200031135-A1.
                Sequence 15 AA;
  24-NOV-1998;
   23-NOV-1999;
   08-NOV-2000
  02-JUN-2000
  AAY92953,
   Query Match
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Gaps

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Length 20; 1; Indels

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RESULT 3

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Synthetic

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The sequences given in AAR82556-57 are myelin basic protein (MBP) derived peptides which were used in the method of the invention for the treatment of multiple sclerosis. These peptides act as bystander antigens and act in combination with an amount of a non-interferon polypeptide having Th2-enhancing cytokine activity
  A set of peptide ligands for agricultural research and development of therapeutic agents comprise specific complementary peptides to proteins encoded by genes of plant genomes.
  Plant; peptide pesticide; peptide herbicide; agricultural research.
 20\, /note= "Indicated in the specification as Cys-NH2"
  Use of oral tolerisation and/or Th2-enhancing cytokine(s)
   Score 32; DB 2; Length 20; Pred. No. 1.4e+02; 5; Mismatches 3; Indels
  auto:immune diseases such as multiple sclerosis.
  Arabidopsis thaliana peptide ligand #102.
  Example 4; Page 45; 201pp; English
   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
  Example 1; Page 33; 49pp; English
  AAG83462 standard; peptide; 10 AA.
   13-DEC-2000; 2000WO-GB004781.
   99GB-00029469.
   95WO-US004512,
   94US-00332524
   94US-00225372
  (first entry)
   4; Conservative
   4 LSFQLGLYLSPH 15
   |:: :|:: ||
LAYTIGVFKDPH 13
   Roberts GW, Heal JR;
  Arabidopsis thaliana.
   WPI; 2001-381629/40.
   (PROT-) PROTEOM LTD.
  Weiner HL, Chen Y;
  WPI; 1995-366229/47
   Query Match
Best Local Similarity
   Sequence 20 AA;
   WO200142279-A2.
   Modified-site
   07-APR-1995;
   08-APR-1994;
   13-DEC-1999;
   31-OCT-1994;
  11-SEP-2001
   19-0CT-1995.
   14-JUN-2001
  AAG83462;
  AAG8346;
  RESULT
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   AAB68429-33 represent peptides derived from a human G-protein coupled receptor, designated HGG7 or MCH-R2. HGG7 is a melanin concentrating hormone receptor. Modulators of HG67 can be used to treat a patient, particularly to reduce weight, particularly in obesity, or to treat stress. These modulators can also be used to treat cancer, reduce pain, treat sexual dysfunction or to produce weight gain. Bringing about weight loss can be used to reduce the likelihood of hypertension, diabetes, dyslipidemia, cardiovascular disease, gall stones, osteoarthritis or certain forms of cancers. Increasing weight can be useful in the treatment of anorexia, AlDS, wasting, cachexia and frail elderly patients, or those undergoing chemotherapy or radiation therapy
                   melanin concentrating hormone receptor; cancer; pain; sexual dysfunction; weight gain; hypertension; dyslipidemia; cardiovascular disease; gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;
G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;
   Myelin basic protein; MBP; multiple sclerosis; MS; bystander antigen; non-interferon polypeptide; Th2-enhancing cytokine activity.
  for
for
  Gaps
  /note= "Indicated in the specification as COOH-Pro"
  New G-protein coupled receptor, designated MCH-R2, is a receptor melanin-concentrating hormone and is useful to provide treatment weight disorders including obesity.
  ö
  Score 32; DB 4; Length 16;
Pred. No. 1.1e+02;
3; Mismatches 2; Indels
  Sano
  Імаава Н,
  Location/Qualifiers
   AAR82557 standard; peptide; 20 AA
  Howard AD,
   Claim 3; Page 32; 32pp; English.
  41.6%;
   14-NOV-2000; 2000WO-US031240.
  16-NOV-1999; 99US-0165871P.
13-MAR-2000; 2000US-0188977P.
18-APR-2000; 2000US-0198029P.
  MERCK & CO INC.
BANYU PHARM CO LTD.
   17-MAY-1996 (first entry)
  6; Conservative
   Bovine PLP peptide 71-90.
  13
  15
  Mcdonald TP,
  3 SLSFQLGLYLS
  WPI; 2001-355618/37.
  Query Match
Best Local Similarity
Matches 6; Conserv
  Sequence 16 AA;
   WO200136479-A1.
  Key
Modified-site
   Homo sapiens.
   25-MAY-2001
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Synthetic

AAR82557;

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Mismatches

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              The present invention relates to a set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is one such peptide from Arabidopsis thaliana. The peptides of the present invention are useful in an assay to identify a peptide, especially a peptide pesticide or herbicide. The peptides are also useful for tools for agricultural research and
  The invention relates to human I kappa B kinase inhibitor 37.40 (ABPS8974) and nucleic acids encoding it (ABZ70827). The protein has a molecular weight of 37.4 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. I kappa B kinase inhibitors 37.40 can be used in the treatment of a variety of diseases such as cancer, angiocardiopathy, neurological disorders, immune disorders and inflammatory conditions. The present sequence represents the 15 N-terminal amino acids of human I kappa B kinase inhibitor 37.40 used in ELISA (enzyme linked immunosorbent assay) in an exemplification of the invention
   Human, I kappa B kinase inhibitor 37.40; recombinant production; gene therapy; cancer; tumour; angiocardiopathy; cardiovascular disorder; neurological disorder; immune disorder; inflammatory condition; cytostatic; antiinflammatory; immunomodulator; N-terminal peptide; enzyme linked immunosorbent assay; ELISA.
   Gaps
  Human inhibitor molecule I kappa B kinase 37.40 polypeptides and polynucleotides encoding this polypeptide.
   ö
  Human I kappa B kinase inhibitor 37.40 N-terminal peptide.
   4; Length 10;
   Indels
   1;
   Example 5; Page 18 (Disclosure); 33pp; Chinese.
   Score 31; DB 4
Pred. No. 98;
2; Mismatches
  (BODE-) BODE GENE DEV CO LTD SHANGHAI.
  $
  ABP58975 standard; peptide; 15
   40.3%;
   26-DEC-2000; 2000CN-00136306
   26-DEC-2000; 2000CN-00136306
   (first entry)
   Conservative
  SLSFOLGLYL 12
  ||:||| |:|
SLTFQLLLFL 10
   Query Match
Best Local Similarity
7; Conserve
   WPI; 2002-751595/82
  Sequence 10 AA;
   Sequence 15 AA;
  Xie Y;
   Homo sapiens
   CN1361264-A.
  14-APR-2003
   development
  31-JUL-2002
   ABP58975;
  Mao Y,
  RESULT 7
  ABP58975
X88888888888
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  The invention relates to an avian pancreatic polypeptide, modified by substitution of at least one amino acid residue, where the residue is being exposed on the alpha helix domain of the polypeptide when the polypeptide is in a tertiary form. The polypeptide is useful for screening drugs to identify agents capable of binding to the same binding site as the avian pancreatic polypeptide. It is also useful for diagnostic purposes to identify the presence and/or detect the levels of DNA or protein that binds to the polypeptide, in treatment of diseases associated with the presence of a particular DNA or protein, where the polypeptide can be used to bind to DNA to promote or inhibit transcription and for identifying binding partners. The present sequence is that of a miniature protein of the invention used to modulate the interaction between a known protein and another molecule
  Polypeptide scaffold e.g. an avian pancreatic polypeptide that comprises modification by substitution of an amino acid residue, that is exposed on the alpha helix domain of the polypeptide is useful for screening for
  Avian pancreatic polypeptide; alpha helix domain; modulate transcription;
  Gapa
   ;
0
  Length 15;
   1; Indels
   Rutledge SE;
  Score 30; DB 5; I
Pred. No. 2.3e+02;
   Zutshi R,
  0; Mismatches
   AAM47809 standard; peptide; 15 AA.
  Example 17; Fig 5; 81pp; English.
  Chin JWK,
Zondlo NJ;
   24-APR-2000; 2000US-019940BP.
16-OCT-2000; 2000US-0240566P.
30-JAN-2001; 2001US-0255099P.
23-FEB-2001; 2001US-0271368P.
   24-APR-2001; 2001WO-US013023.
  39.0%;
85.7%;
  (first entry)
  6; Conservative
 13
  Schepartz Shrader A,
Kehlbeck Martin JD,
                           s Frigiris 12
   Miniature protein 9.
   FQLGLYL 12
   WPI; 2002-041395/05
  Local Similarity
FOLGLYLS
  miniature protein
   (UYYA ) UNIV YALE
  Sequence 15 AA;
  WO200181375-A2.
  15-FEB-2002
   01-NOV-2001
   Synthetic
   AAM47809;
   ø
   Query Match
   drugs
   - Matches
   RESULT 8
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FOLGWYL

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RESULT

Length 15;

Score 31; DB 5; Pred. No. 1.5e+02;

40.3%;

Query Match Best Local Similarity ហ

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Pred. No. 2.7e+02;

45.5%;

```
The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful in detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for creating immune-related diseases, growth-related diseases, call seases, careation immune diseases, growth-related diseases, call sease, atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, seteboprossis, cancer, cardiomyopathy, chronic and acute disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42283 to ABZ42869 encode GPCR proteins given in ABS81675 to ABZ42289 encode ceremonal and content invention.
   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity, nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
   New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
   G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1221
                             ABP82548 standard; peptide; 17 AA.
  (LIFE-) LIFESPAN BIOSCIENCES INC.
  Brown JP;
  Claim 1; Fig 2; 523pp; English.
  19-DEC-2000; 2000US-0257144P.
  19-DEC-2001; 2001WO-US050107.
   04-MAR-2003 (first entry)
  Roush CL,
   WPI; 2003-046718/04.
   autoimmune diseases.
  À,
  WO200261087-A2
   Homo sapiens.
   Sequence 17
   08-AUG-2002
  Burmer GC,
  ABP82548;
ABP82548
ID ABP8
```

```
A pure 3-phosphoinositide-dependent protein kinase (3PDPK) that phosphorylates and activates PK B-alpha has been isolated. The present sequence represents a rabbit 3-phosphoinositide dependent protein kinase peptide. Products from the present invention (e.g. 3PDPK, nucleotide sequence encoding 3PDPK, antibodies against 3PDPK) can be used to diabentify compounds which modulate the PK activity e.g. for treating diabetes or cancers or for enhancing cell proliferation in the regeneration of nerves or in wound healing
  Gaps
                 Gaps
   New isolated 1-phosphoinositide-dependent protein kinase - which phosphorylates and activates protein kinase B-alpha, used to develop products for treating diabetes or cancers or for enhancing cell
  Protein kinase B-alpha, 3-phosphoinositide-dependent protein kinase, diabetes, cancer, cell proliferation, phosphorylation.
  .
0
                ö
  Rabbit 3-phosphoinositide dependent protein kinase peptide. #5.
   39.0%; Score 30; DB 2; Length 21; 70.0%; Pred. No. 3.48+02; ive 1; Mismatches 2; Indels
                4; Indels
                2; Mismatches
  Example 2; Page 57; 120pp; English.
   AAE09350 standard; protein; 23 AA.
   AAW71733 standard; peptide; 21 AA.
  97GB-00005462.
97GB-00012826.
97GB-00017253.
97US-00943667.
   98WO-GB000777
   (MEDI-) MEDICAL RES COUNCIL.
   (first entry)
   Conservative
              5; Conservative
  1 IDSLSFQLGL 10
  Oryctolagus cuniculus.
  ||| |:: |
SFQKSFYINAH
   5 SFQLGLYLSPH
   Query Match
Best Local Similarity
7; Conserv
   WPI; 1998-531572/45.
  LDSNSFELDL
Best Local Similarity
Matches 5; Conserv
  Sequence 21 AA;
   proliferation.
  WO9841638-A1
   10-DEC-1998
  16-MAR-1998;
  17-MAR-1997;
19-JUN-1997;
  03-OCT-1997;
  15-AUG-1997;
  24-SEP-1998
   Alessi DR;
  AAW71733;
  12
  AAE09350
   RESULT 11
   RESULT 10
  AAE09350
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DB 6; Length 17;

39.0%; Score 30;

Query Match

```
Human ion channel-72 (ion72) protein.
  protein from human
   Query Match
Best Local Similarity
  N-PSDB; AAD17149
  Sequence 23 AA;
  WO200168849-A2
   Homo sapiens.
  10-MAR-2000;
   06-JUL-2000;
  20-SEP-2001.
   ABU97358;
  н
   Wood LS,
   Wang J,
  Matches
  RESULT 13
  ABU97358
  ò
  ద
   XXXEX
   ö
  The present sequence is human ion channel-10 (ion-10) protein. The invention relates to human ion channel polypeptides and nucleic acid molecules encoding such polypeptides. The ion channel proteins are useful targets for discovering ilgands or drugs to treat discorders or defects, including schizophrenia, depression, anxiety, attention deficit hyperactivity discorder (ADHD), migraine, stroke, ischaemia, respiratory diseases (e.g. asthma), brain injury, neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease, glaucoma and macular degeneration. Compounds which modulate ion channel proteins are used in the treatment of cardiovascular diseases including congestive heart failure, arrhythmia, high blood pressure, restenosis, endocrine disorders (e.g. cardors), spliepsy, proliferative disorders (e.g. cancer), bipolar and other mood disorders, inflammatory conditions, autoimmune
   channel proteins are used as research tools for identification, characterisation and purification of interacting regulatory proteins. Ion channel cDNAs are used in gene therapy
  New ion channel polypeptides and polynuclectides encoding them, for treating e.g. schizophrenia, depression, anxiety, attention deficit hyperactivity disorder, migraine, stroke, ischemia, respiratory diseases.
  disorders, muscular disorders, obesity and retinal degeneration. The ion channel proteins are used as research tools for identification,
   Gaps
   Human; ion channel-10; ion-10; schizophrenia; depression; anxiety; attention deficit hyperactivity disorder; ADHD; migraine; stroke; ischaemia; respiratory disease; asthma; neurodegenerative disease; Alzheimer's disease; arrhythmia; cancer; macular degeneration; cardiovascular disease; endocrine disorder; congestive heart failure; thyroid disorder; inflammatory condition; epilepsy; muscular disorder; autoimmune disorder; mood disorder;
   ..
0
   Score 30; DB 4; Length 23;
Pred. No. 3.8e+02;
3; Mismatches 3; Indels
  Ruble CL;
   Claim 35; Page 67; 108pp; English.
  AAE10097 standard; protein; 23 AA.
  (PHAA ) PHARMACIA & UPJOHN CO.
  14-FEB-2001; 2001WO-US004644.
   14-FEB-2000; 2000US-0182325P
   39.0%;
50.0%;
  Karnovsky AM,
19-NOV-2001 (first entry)
  29-NOV-2001 (first entry)
  6; Conservative
   1 LDSLSFOLGLYL 12
  | | :| ||:|
LDLVSCVLGIYI 20
                           Human ion-10 protein.
  WPI; 2001-536567/59.
N-PSDB; AAD16151.
  Query Match
Best Local Similarity
Matches 6; Conserv
  Sequence 23 AA;
   WO200160864-A2
  Homo sapiens.
   therapy
  Roberds SL,
  23-AUG-2001
  AAE10097;
  gene
  RESULT 12
   AAE10097
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  ð
   XHXK
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Human; ion channel-72; ion72; antiinflammatory; immunosuppressive; analgesic; noctropic; neuroprotective; antidepressant; cardiant; cytostatic; antiviral; human immunodeficiency virus; HIV; anorectic; antiviral; thyroid disorder; thyrotoxicosis; myxoedems; renal failure; Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke; psychotic disorder; neurological disorder; anxiety; dyskinesia; Huntington's disease; degenerative disorder; Parkinson's disease; schizophrenia; Alzheimer's disease; cardiovascular disease; cancer; metabolic disorder; anorexia; obesity; mental disorder.
   The patent discloses novel human ion channel polypeptides and their corresponding polymucleotides. The ion channel sequences and their modulators are used for the treatment of viral infections (e.g. human immunodeficiency virus (HIV)), thyroid discrete (e.g., thyrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g., tryrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g., Crobn's discase), and neurological disorders (e.g. anxiety, depression and schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative discorders (e.g., Parkinson's disease, Alzheimer's disease), cardio-vascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity) and mental disorders. The present sequence is ion channel-72 (ion72)
   Gaps
   Linske-O'connell LI;
   New ion channel polynucleotides and polypeptides, useful for identification of ion channel modulators and treatment of mental disorders, infections, cancer and autoimmune diseases.
   .
0
  Length 23;
   3; Indels
  Score 30; DB 4; I
Pred. No. 3.8e+02;
3; Mismatches 3;
   Karnovsky AM, Ruble CL,
  Ś
   English.
  ABU97358 standard; peptide; 23
  (PHAA ) PHARMACIA & UPJOHN CO.
   10-MAR-2000; 2000US-0188517P.
10-MAR-2000; 2000US-0188518P.
10-MAR-2000; 2000US-0188519P.
05-JUL-2000; 2000US-0215815P.
   2000US-0216481P
  09-MAR-2001; 2001WO-US007503
  39.0%;
   Claim 31; Page 93; 188pp;
  29-JUL-2003 (first entry)
   6; Conservative
  LDSLSFQLGLYL 12
  || :| ||:|:
LDLVSCVLGIYI 20
  Vogeli G,
Liu D;
   2001-565795/63.
```

Composite binding polypeptide; zinc finger nucleic acid binding domain; autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;

Human zinc finger DNA binding domain #318.

(first entry)

25-AUG-2003

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ð
   infections, inflammatory conditions (e.g. Crohn's disease), diseases related to homeostasis, rheumatoid arthritis, autoimmune disorders, central nervous system (CNS) disorders (e.g. dementia, Huntington's disease), degenerative disorders (e.g. Parkinson's and Alzheimer's disease), cardiovascular diseases (e.g. myocardial infarction), cancer, and hormonal disorders. The polynucleotide sequences are useful to design novel transcription factors for modulating the expression of human ion polypeptides in native cells, and cells transformed or transfected with them. The present sequence represents an amino acid sequence encoded by a
   The present invention relates to the isolation of novel human ion channel polypeptides, and the polynuclectide sequences encoding them. The human ion channel polypeptides are useful for inducing an immune response in a mammal, and for identifying a compound which binds to and/or modulates the ion channel. The polynuclectide sequences encoding human ion channel polypeptides are useful for screening restriction fragment length polymorphisms (RPLPs) associated with certain disorders, and for genetic polymorphisms (RPLPs) associated with certain disorders, and for genetic
  mapping. The human ion channel polypeptide and polynucleotide sequences are useful in the treatment of diseases or conditions such as viral
  oolypeptide, useful for inducing an immune for treating disease or conditions related to
  restriction fragment length polymorphism; viral infection; inflammatory condition; Crohn's disease; homeostasis; cancer; cheumatoid arthritis; autoimmune disorder; CNS disorder; dementia; central nervous system disorder; Huntingron's disease; virucide; degenerative disorder; Parkinson's disease; Alzheimer's disease; cardiovascular disease; myocardial infarction; hormonal disorder; transcription factor; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; nootropic, anticonvulsant; antiparkinsonian;
   ion channel; immune response; RFLP; genetic mapping;
Amino acid sequence for human ion channel cDNA clone Ion72.
   Length 23;
  Ruble CL;
  Score 30; DB 6; I
Pred. No. 3.8e+02;
}; Mismatches 3;
  Roberds SL, Benjamin CW, Karnovsky AM,
   Novel human ion channel polypeptide,
   Example 3; Page 97; 146pp; English.
  central nervous system and cancer.
   (PHAA ) PHARMACIA & UPJOHN CO.
  12-SEP-2001; 2001US-0318733P.
   12-SEP-2002; 2002WO-US029087.
  13-AUG-2002; 2002US-0403254P.
   39.0%;
  human ion channel cDNA clone
  neuroprotective; cardiant
  response in a mammal and
   WPI; 2003-313250/30.
   N-PSDB; ACD01534
   WO2003023014-A2.
  Sequence 23 AA;
  Homo sapiens
  20-MAR-2003
   Query Match
```

New composite binding zinc finger polypeptide, useful for designing sequence-specific binding proteins regulating gene expression in the fields of molecular biology, and for the diagnosis and treatment of

Example 2; Page 78; 157pp; English.

autoimmune disorders.

Moore M, Sepp A, Isalan M, Choo Y;

WPI; 2003-278214/27.

(SANG-) SANGAMO BIOSCIENCES INC.

04-APR-2002; 2002WO-US022272. 04-APR-2001; 2001GB-00008491.

WO200299084-A2.

12-DEC-2002,

Homo sapiens.

human.

```
The invention relates to a composite binding polypeptide comprising a first natural binding domain derived from a first natural binding polypeptide and second natural binding domain derived from a first natural binding polypeptide, where the first and second natural binding polypeptide, where the first and second natural binding polypeptides. The invention also relates to a changer of polypeptides. The invention also relates to a changer of second binding polypeptides. The invention also relates to a changer of polypeptide comprising a binding polypeptide cited above and a biological effector domain, a library of natural binding domains. A library of catached to it, a method for selecting a binding polypeptide capable of binding to a target site and a method for designing a composite binding polypeptide. The methods and compositions of the present invention are useful for designing sequence-specific binding proteins for regulation of the diagnosis and transgenic animals of a method disorders, and as research tools and in transgenic animals. This sequence represents a human zinc finger DNA binding domain used in the scope of the invention
  ö
  nootropic; neuroprotective; neuroleptic; immunosuppressive; cardiant;
   Gaps
  ..
0
   39.0%; Score 30; DB 6; Length 23; 45.5%; Pred. No. 3.8e+02; tive 4; Mismatches 2; Indels
   Novel human ion channel ion-72 protein.
  ADE29276 standard; protein; 23 AA.
   (first entry)
  5 SFQLGLYLSPH 15
   ||: |::|: |
SFRQGMHLTRH
   Sequence 23 AA;
   29-JAN-2004
  ADE29276;
   ADE29276
  임
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Gaps ö

3; Indels

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6; Conservative 1 LDSLSFQLGLYL 12 || :| ||:|: 9 LDLVSCVLGIYI 20

Matches

Local Similarity

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ABO12018 standard; peptide; 23

RESULT 14 AB012018

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AB012018;

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New nucleic acid sequences encoding ion channels are useful to detect and treat human diseases and conditions, particularly of the brain,
        opthalmological; cytostatic; hypertensive; hypetensive; vasorropic; antimigraine; analgesic, antiparkinsonian; thrombolytic; antithyroid; ion channel; ion-x; brain disorder; mental disorder; schizophrenia; depression; anxiety; attention deficit hyperactivity disorder; migraine; stroke; neurodegenerative disease; Alzheimer's disease; astronous disease; abaucoma; macular degeneration; cardiovascular disease; ischaemia, congestive heart failure; arrythmia; high blood pressure; restenoiss; thyroid disorder; renal failure; high blood pressure; restenoiss; thyroid disorder; renal failure; movement disorder; central nervous system disorder; infection; eating disorder; cardiovascular disorder; thromboais; atherselerosis; proliferative disorder; cancer; hormonal disorder; sexual dysfunction.
 antiarteriosclerotic; antiinflammatory; antidepressant; antiarthritic;
  Ruble CL;
   Roberds SL, Benjamin CW, Karnovsky AM,
Linske-O'connell LI, Wang J, Liu D;
   Claim 31; SEQ ID NO 79; 105pp; English.
  10-MAR-2000; 2000US-0188484F.
10-MAR-2000; 2000US-018851FP.
10-MAR-2000; 2000US-0188518F.
10-MAR-2000; 2000US-0188519F.
05-UUL-2000; 2000US-0215815F.
06-UUL-2000; 2000US-0215815F.
  ROBERDS S.
BENJAMIN C W.
KARNOVSKY A M.
RUBLE C L.
LINSKE-O'CONNELL I.
  09-MAR-2001; 2001US-00802668
  especially mental disorders.
  WPI; 2003-875311/81.
N-PSDB; ADE29225.
  US2003190714-A1
  LIU D.
  Homo sapiens.
  10-MAR-2000;
  09-OCT-2003
  (LINS/)
(WANG/)
   ROBE/)
  (BENJ/)
  RUBL/)
```

particularly mental disorders, including schizophrenia, depression, anxiety, attention deficit hyperactivity disorder, migraine, stroke, and neurodegenerative diseases such as Alzheimer's disease, parkinson's disease, glaucoma and macular degeneration, cardiovascular diseases such as ischaemia, congestive heart failure, arrythmia, high blood pressure as ischaemia, congestive heart failure, arrythmia, high blood pressure disorders, renal failure, inflammatory conditions, autoimmune disorders including rheumatoid arthritis, movement disorders, central nervous system disorders, infections, eating disorders, cardiovascular disorders including thrombosis and athersclerosis, and proliferative disorders such as cancers, hormonal disorders and sexual dysfunction. This is the amino acid sequence of a novel ion channel. The invention describes an isolated nucleic acid comprising a sequence encoding at least a portion of an ion channel (ion-x). The invention is useful to detect and treat diseases and conditions of the brain,

Sequence 23 AA;

Query Match
39.0%; Score 30; DB 7; Length 23;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels

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Gaps . 0

| | : | | | : | 9 LDLVSCVLGIYI 20

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Search completed: November 14, 2004, 12:02:18 Job time : 45.4043 secs

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November 14, 2004, 12:03:21; Search time 35.4255 Seconds (without alignments) 149.815 Million cell updates/sec
  FUDILIBRICA APPLICATIONS AND TO THE COME. PEPT 1. (1972 6/ptodata/1/pubpaa/USO7 PUBCOMB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO7 PUBCOMB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO6_PUBGOMB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO6_PUBGOMB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO7_NEW PUB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO8 PUBCOMB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO9 NEW PUB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO0 PUBCOMB. PEPT 1. (1972 6/ptodata/1/pubpaa/USO0 NEW PUB. PEPT 1. (1972 6/ptodata/1/pubp
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
   1568699 seqs, 353819137 residues
  Published Applications AA:*
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   OM protein - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   1 LDSLSFQLGLYLSPH 15
  US-09-831-253F-9
   Minimum DB seq length: 0 Maximum DB seq length: 23
  Title:
Perfect score:
   Scoring table:
   Database :
   Sequence:
   Searched:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|      | Description              | Sequence 102, App  | Sequence 55, Appl | Sequence 98, Appl | Sequence 55, Appl | Sequence 98, Appl | Sequence 55, Appl | Sequence 98, Appl | Sequence 1221, Ap   | Sequence 12, Appl | Sequence 79, Appl | Sequence 79, Appl | Sequence 2145, Ap  | Seguence 2145. Ap  |
|------|--------------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|-------------------|--------------------|--------------------|
|      | ΩΙ                       | US-09-572-270A-102 | US-10-682-420-55  | US-10-682-420-98  | US-10-409-613-55  | US-10-409-613-98  | US-10-442-180-55  | US-10-442-180-98  | US-10-225-567A-1221 | US-10-190-012-12  | US-09-802-668-79  | US-10-243-475-79  | US-09-880-748-2145 | US-10-293-418-2145 |
|      |                          |                    |                   |                   |                   |                   |                   |                   |                     |                   |                   |                   | 10                 |                    |
|      | Query<br>Match Length DB | 10                 | 15                | 15                | 15                | 15                | 15                | 15                | 17                  | 21                | 23                | 23                | 16                 | 16                 |
| dip. | Query<br>Match           | 40.3               | 39.0              | 39.0              | 39.0              | 39.0              | 39.0              | 39.0              | 39.0                | 39.0              | 39.0              | 39.0              | 38.3               | 38.3               |
|      | Score                    | 31                 | 30                | 30                | 30                | 30                | 30                | 30                | 30                  | 30                | 30                | 30                | 29.5               | 29.5               |
|      | Result<br>No.            | -                  | 7                 | ٣                 | 4                 | 2                 | 9                 | 7                 | æ                   | σ                 | 10                | 11                | 12                 | 13                 |

| Sequence 26, Appl Sequence 297, App Sequence 101, App Sequence 319, App Sequence 319, App Sequence 99, Appl Sequence 2062, App Sequence 2062, App Sequence 2062, App Sequence 2062, App Sequence 2063, App Sequence 2064, App Sequence 211, App Sequence 31, Appl Sequence 611, App |            |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|
| US-10-197-954-26 US-09-974-879-297 US-09-818-683-297 US-09-818-683-297 US-09-818-683-297 US-09-818-683-297 US-10-424-599-180905 US-10-621-401-297 US-10-119-536A-101 US-10-621-266-758 US-10-682-426-919 US-10-682-420-99 US-10-10-682-420-99 US-10-10-682-420-99 US-10-10-1179 US-10-225-567A-2058 US-10-225-264 US-10-225-264 US-10-225-264 US-10-235-499-13 US-10-235-471-611 US-10-253-471-611                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ALIGNMENTS |
| 4 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |
| 11<br>233333333333333333333333333333333333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |            |
| C $C$ $C$ $C$ $C$ $C$ $C$ $C$ $C$ $C$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            |
| <u>-</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |
| 777777777788888888888888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | •          |
| 4 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |            |

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Sequence 102, Application US/09572270A
; Sequence 102, Application US/09572270A
; Publication No. US20030148368A1
; Publication No. US20030148368A1
; Publication No. US20030148368A1
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT FILING DATE: 2000-05-17
; SEQ ID NO 102
; SEQ ID NO 102
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in ILL2. at 8-17 and may interact with
   Gaps
   ö
  40.3%; Score 31; DB 10; Length 10; 70.0%; Pred. No. 1.2e+02; tive 2; Mismatches 1; Indels
  RESULT 2
US-10-682-420-55
Sequence 55, Application US/10682420
Publication No. US2004006775A1
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
   Query Match
Best Local Similarity 70...
Best Local 3; Conservative
   ||:||| |:|
SLTFQLLLFL 10
  3 SLSFQLGLYL 12
  US-09-572-270A-102
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ORGANISM: Type B PWD circovirus US-10-409-613-55
  Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
                          2 VNELRFNIGOFLPP 15
   VNELRFNIGOFLPP 15
  1 LDSLSFQLGLYLSP 14
   SEQ ID NO 55
LENGTH: 15
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  a
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  δ
  APPLICANT: ALBINA, Emanuel
APPLICANT: ALBINA, Emanuel
APPLICANT: BLANCHARD, Phillipe
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HITET, Verlyne
APPLICANT: HANAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: MABE, Dominique
APPLICANT: MABER: US/10/682,420
CURRENT APPLICATION NUMBER: US/10/637,011
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Version 3.0
   ö
   TITLE OF INVENTION: CIRCOLIANS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS TITLE OF INVENTION: DISEASE (PWD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/682,420
CURRENT PILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-10-08-08
PRIOR FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US/09/514,2458
PRIOR APPLICATION NUMBER: By 97/15396
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR PLING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATCHIN VORS: 170
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  Length 15;
  Query Match 39.0%; Score 30; DB 15; Length 15; Best Local Similarity 35.7%; Pred. No. 2.8e+02; Matches 5; Conservative 4; Mismatches '5; Indels
  Score 30; DB 15; Length 15
Pred. No. 2.8e+02;
4; Mismatches 5; Indels
  Sequence 98, Application US/10682420 Publication No. US20040062775A1 GENERAL INFORMATION: APPLICANT: JESTIN, Andre
   TYPE: PRT (CRGANISM: Type A PWD circovirus US-10-682-420-98)
   ) ORGANISM: Type B PWD circovirus US-10-682-420-55
                HUTET, Evelyne
ARNAULD, Claire
TRUONG, Catherine
   Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
   MAHE, Dominique
CARIOLET, Roland
  2 VNELRFNIGQFLPP 15
  1 LDSLSFQLGLYLSP 14
   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT FILING DATE: 2003-05-21
FINIOR APPLICATION NUMBER: US/09/514,245
FRIOR FILING DATE: 2000-02-28
FRIOR PILING DATE: 1990-112-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SOCITWARE: Patentin version 3.0
   ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
   ) TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-442-180-98
  :: | | :| :| | vNELRFNIGQFLPP 15
  1 LDSLSFQLGLYLSP 14
   Query Match
Best Local Similarity 35...
Best Local Similarity 5...
   Query Match
Best Local Similarity 45.5.
Then 5; Conservative
   ||| |:: |
2 SFQKSFYINAH 12
  S SFOLGLYLSPH 15
  TYPE: PRT
ORGANISM: Homo sapiens
  US-10-225-567A-1221
   JS-10-225-567A-1221
   RESULT 9
US-10-190-012-12
   SEQ ID NO 1221
   ઠ
   셤
   ò
   d
  APPLICANT: TRUONG, Claire
APPLICANT: TRUONG, Claire
APPLICANT: TRUONG, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MALE, Dominque
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PWD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT FILING DATE: 2003-05-21
PRIOR PILING DATE: 2000-02-28
PRIOR PILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO 55
LENGTH: 15
   Sequence 98, Application US/10442180
Sequence 98, Application US/20040091502A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: LESTIN, Philipe
APPLICANT: HUTET, Evelyne
APPLICANT: HUTET, Evelyne
APPLICANT: RANGULD, Claire
APPLICANT: RANGULD, Claire
APPLICANT: MAHE, Dominique
APPLICANT: MAHE, Dominique
APPLICANT: MADEC, Prancois
, ROLANG
APPLICANT. MADEC, PRANCOIST, R
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   ö
  Gaps
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   Score 30; DB 15; Length 15;
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  ALBINA, Emanuel
Le CANN, Pierre
BLANCHARD, Phillipe
HUTET, Evelyne
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US-10-409-613-98
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Similarity 35.7%;
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   2 VNELRFNIGQFLPP 15
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Best Local Similarity
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LENGTH: 15
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APPLICANT:
  TYPE: PRT
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  ઠે
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Sequence 121, Application US/1022567A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
FRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
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39.0%; Score 30; DB 15; Length 15; 35.7%; Pred. No. 2.8e+02; ive 4; Mismatches 5; Indels
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  4; Indels
  Sequence 12, Application US/10190012
; Publication No. US20030108971A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: ENZYME
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacckle Fleischmann & Mugel, LLP
STREET: 39 State Street
; CITY: Nochester
; STRIET: New York
; COUNTRY: USA
  Pred. No. 3.2e+02;
2; Mismatches 4
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   FULLCALION NO. US.7003003937A1

FULLCAUT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FULE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

FURENT FILING DATE: 2001-06-15

FRIOR APPLICATION NUMBER: 60/212,210

FRIOR PILING DATE: 2000-06-15

FRIOR PILING DATE: 2000-10-17

FRIOR PILING DATE: 2001-03-16

FRIOR PILING DATE: 2001-03-16

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FRIOR FILING DATE: 2001-03-16

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-05-25
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38.3%; Score 29.5; DB 10; Length 16;
Best Local Similarity 61.5%; Pred. No. 3.6e+02;
Matches 8; Conservative 2; Mismatches 2; Indels
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   3; Indels
   Sequence 79, Application US/10243475; Sequence 79, Application US/20030194720A1
GENERAL INPORMATION:
APPLICANT: Roberds, Steven L.
APPLICANT: Renjamin, Christopher W.
APPLICANT: Ranovsky, Alla M.
APPLICANT: Ranovsky, Alla M.
APPLICANT: RANDLE, Cara L.
TITLE OF INVENTION: Human Ion Channels FILE REFERENCE: PHRW0039-100
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: 60/403,254
PRIOR PELING DATE: 2002-08-13
PRIOR FILING DATE: 2002-08-13
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 138
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LDLVSCVLGIYI 20
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Best Local Similarity
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US-10-243-475-79
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/190,012
FILING DATE: 05-Jul-2002
CIASSIFICATION: 'Unknown>
PRIOR APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
ATTORNEY AGENT: INFORMATION:
ATTORNEY/AGENT: INFORMATION:
  39.0%; Score 30; DB 14; Length 21; 70.0%; Pred. No. 4e+02; tive 1; Mismatches 2; Indels
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  NAME: Braman, Susan J
REGISTRATION NUMBER: 34, 103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
   SQUENCE 79, Application US/09802668
| Publication No. US20030190714A1
| GENERAL INFORMATION:
| APPLICANT: Wood. Linda
| APPLICANT: Wogeli, Gabriel
| APPLICANT: Karnovsky, Alla
| APPLICANT: Linda | APPLICANT: Wang, Jun
| APPLICANT: Wang, Jun
| APPLICANT: Wang, Jun
| APPLICANT: Wang, Jun
| APPLICANT: Wang, Jun
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| APPLICANT: Wang, Jun
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| APPLICANT: Wang, Jun
| TITLE REFERENCE: 00069US.
| CURRENT APPLICATION NUMBER: 6/188,517
| PRIOR PILING DATE: 2000-03-10
| NUMBER OF SEQ ID NOS: 117
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CORGANISM: Homo sapiens
US-09-802-668-79
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Publication No. US20030028003A1
GENERAL INFORMATION: 125 Human Secreted Proteins
FITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
FURIOR APPLICATION NUMBER: US 60/239,893
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-11-04
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PRIOR PRILING DATE: 1997-11-17
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ORGANISM: Homo sapiens
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US-10-197-954-26
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  ઠ
  papelicant: Rieter, Hubert

APPLICANT: Siddigi, Suhaib

TITLE OF INVENTION: Capture Compounds, Collections Thereof

TITLE OF INVENTION: Compositions

TITLE OF INVENTION: Compositions

TITLE OF INVENTION: Compositions

FILE OF INVENTION: Compositions

TITLE OF INVENTION: Compositions

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FILE OF INVENTION: Compositions

FILE OF INVENTION: Compositions

FRICK RPLICATION NUMBER: US/10/197,954

CURRENT FILING DATE: 2001-07-16

PRIOR FILING DATE: 2001-08-21

PRIOR FILING DATE: 2001-08-21

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 149

SOFTWARE: FASESEQ for Windows Version 4.0
   Gaps
  JARGARA INFORMATION:

JARLANDEL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FRIOR PELING DATE: 2002-11-27

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-12-19

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

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Publication No. US20030223996A1
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Publication No. US20030119021A1
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Best Local Similarity
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Search completed: November 14, 2004, 12:27:00 Job time : 35.4255 secs

us-09-831-253f-9.rapb

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  GENERAL INFORMATION:

APPLICANT: Liu, Qingyun
APPLICANT: Howard, Andrew D.
APPLICANT: Howard, Andrew D.
APPLICANT: Howard, Hisashi
APPLICANT: Howard, Hisashi
APPLICANT: Sano, Hideki
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 20579Y
CURRENT APLICATION NUMBER: US/09/712,368
CURRENT FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/165,871
PRIOR PILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/188,977
PRIOR PILING DATE: 2000-03-13
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PRIOR PILING DATE: 2000-03-13
SRIOR PILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE FEATERQ FOR WINDOWS Version 4.0
SEQ ID NO 9
LENGTH: 16
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US-09-514-245-55
is Sequence 55, Application US/09514245
js Patent No. 6703023
igeneral INFORMATION:
js APPLICANT: JESTIN, Andre
js APPLICANT: Le CANN, Pierre
js APPLICANT: BLANCHARD, Phillipe
js APPLICANT: HUTBT, Evelyne
js APPLICANT: HUTBT, Evelyne
js APPLICANT: ARNAULD, Claire
   ; Sequence 9, Application US/09712368; Patent No. 6593108; GENERAL INFORMATION:
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Sequence 1855, Appl
Sequence 1944, Appl
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Sequence 1867, Appl
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12, Appl
12, Appl
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18, Appl
240, App
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9, Appl
1955, Appl
1185, Appl
620, Appl
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84.242 Million cell updates/sec
   November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds
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US-09-514-245-55

US-09-514-245-98

US-08-93-667-19

US-08-73-7508-64

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US-09-1245-99

US-09-1245-99

US-09-490-153-240

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Database

Result No.

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RESULT 5
US-08-753-750B-64

i Sequence 64, Application US/08753750B

partent No. 6610506

GENERAL INFORMATION:
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Bother, Andrew A.
TITLE OF INVENTION: PASTEURELIA HARMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENTION: PASTEURELIA HARMOLYTICA AND VACCINES CONTAINING THE SAME
FILE REFERENCE: A34762 021645.0105

CURRENT APPLICATION NUMBER: US/08/753,750B

CURRENT APPLICATION NUMBER: CA 2,164,274

PRIOR PILING DATE: 1995-11-01

PRIOR FILING DATE: 1995-12-01

PRIOR FILING DATE: 1995-12-01

PRIOR FILING DATE: 1995-12-01

PRIOR FILING DATE: 1995-12-01

NUMBER OF SEQ ID NOS: 68

SOFTHARE: FREESE FREESE FREESE FOR Windows Version 4.0
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   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
Fleischmann & Mugel, LLP
  1; Mismatches
  NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMINICATION INFORMATION:
TELEPHONE: 716-262-3640
   CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNDERS:
FILING DATE: 17-MAR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 971253.0
FILING DATE: 15-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
  TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
  ADDRESSEE: Jaeckle Flei.
STREET: 39 State Street
CITY: Rochester
   Query Match
Best Local Similarity 70.0
Matches 7; Conservative
  internal
  TOPOLOGY: Linear
MOLECULE TYPE: peptide
   1 LDSLSFQLGL 10
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   14614-1310
   New York
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FRAGMENT TYPE:
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  12
   ò
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                                      APPLICANT: MADEC, Frances
TITLE OF INVENTION: CIRCOVINUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
FILE REFERENCE: 065691/0106
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
FRIOR PRICH RILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO S5
LENGTH: 15
TYPE: PAT
ORGANISM: Type B PWD circovirus
US-09-514-245-55
  TILLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILLING DATE: 2000-02-28
PRIOD ADDITORATION TO ALLOS ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
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Pred. No.
  PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
  Sequence 12, Application US/08943667; Patent No. 6734001; GENERAL INFORMATION: APPLICANT: Alessi, Dario R TITLE OF INVENTION: BNZYME; NUMBER OF SEQUENCES: 35
  Sequence 98, Application US/09514245 Patent No. 6703023
  APPLICANT: ALBINA, Emanuel
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: HUTET, Evelyne
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: RNONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: MAHE, Dominique
APPLICANT: MAHE, Dominique
APPLICANT: MAHE, Dominique
APPLICANT: MABEC, Francois
TITLE OF INVENTION: CIRCOVIRUS
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US-09-514-245-98
  39.0%;
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MAHE, Dominique
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Matches 5; Conservative
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5; Conservat
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  US-09-514-245-98
   NUMBEL
SOFTWARE:
SEQ ID NO 98
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APPLICANT:
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STATE: New York
COUNTRY: USA
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2; Mismatches 1; Indels
   DB 3; Length 17;
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  APPLICANT: Yabuta, Masayuki
APPLICANT: Yabuta, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
  Version #1.30
   Score 29; DB 3
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  CURRENT APPLICATION DATA:
SOFTWARE:
PAGENTIN Release #1.0, Versi
SOFTWARE:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05.28F-1995
CLASSIFICATION DATA:
APPLICATION DATA:
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APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-58F-1994
PRIOR APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-80V-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meath, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
TELECOMMUNICATION INFORMATION:
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  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 18, Application US/08523373
Patent No. 6037145
; GENERAL INFORMATION:
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Matches 5; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  2 IEDIHFELRLYRRHH 16
   1 LDSLSFQLGLYLSPH 15
   MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-7508-64
  Query Match 37.7
Best Local Similarity 66.7
Matches 6; Conservative
  TELEPHONE: 703-02
TELEPHONE: 703-836-2021
   4 SESWELGLY 12
  3 SLSFQLGLY 11
  linear
  USA
  COUNTRY:
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US-09-514-245-99

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CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEAS
   ö
   Gaps
   ö
  DB 4; Length 15; 58;
  4; Indels
   E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
  APPLICANT: Rapplk, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plucekthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESSOUDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
   CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AGG-1995
ATTORNEY/AGRIT INFORMATION:
NAME: James F. Haley, Jr., Esg.
REGISTRATION NUMBER: 27,794
   2; Mismatches
  FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FF 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
  Score 28;
Pred. No. 5
   REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
  Sequence 240, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
  ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PG-DOS/MS-DOS
Sequence,
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: REALCOGIB
   SEQ ID NO 99
LENGTH: 15
TYPE: PRT
OCCAMISM: Type A PWD circovirus
US-09-514-245-99
  36.4%;
   APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCO
  Query Match 36.4
Best Local Similarity 45.5
Matches 5; Conservative
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1 LRFNIGQFLPP 11
   4 LSFQLGLYLSP 14
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OLGLYLSPH 15
   3 RLQAYLKPH 11
  US-09-490-153-240
   US-09-490-153-240
   US-07-990-893-9
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   Gaps
   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EACOMPY disk
COMPUTER: IMP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 24-Jan-2000
PRIOR APPLICATION WUMBER: PS 5 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
   ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
   ö
   US-09-490-070A-240

| Sequence 240 Application US/09490070A
| Sequence 240 Application US/09490070A
| Pacer No. 6696248
| Pacer No. 6696248
| Pacer Pa
   36.4%; Score 28; DB 4; Length 17; 55.6%; Pred. No. 67; 1; Mismatches 3; Indels
  Query Match
36.4%; Score 28; DB 3; Length 17;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 3; Indels
   DESCRIPTION: SEQ ID NO: 240:
   TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
   STRANDEDNESS: <Unknown>
  LENGTH: 17 amino acids
   240:
  INFORMATION FOR SEQ ID NO: 240
   SEQUENCE CHARACTERISTICS
  TYPE: internal
  TOPOLOGY: linear
ULE TYPE: protein
   CITY: Washington
STATE: D.C.
COUNTRY: USA
(212) 596-9090
   17 amino acids
   Query Match
Best Local Similarity 55.6
Matches 5, Conservative
  TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
  :| || ||
3 RLQAYLKPH 11
   7 OLGLYLSPH 15
   LENGTH: 17 amino
TYPE: amino acid
STRANDEDNESS:
   ;
US-09-490-070A-240
  US-09-025-769B-240
  FRAGMENT
   셤
   ò
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Gарв
   ..
0
   CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
   COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
   Length 17;
   3; Indels
Sequence 240, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION: Knapplk, Achim
APPLICANT: Knapplk, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
   Score 28; DB 4;
Pred. No. 67;
  APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
   NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REPERBNICAL NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
   Mismatches
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
  TOPOLOGY: linear
MOLECULE TYPE: protesin
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 240:
   COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  Sequence 9, Application US/07990893
Patent No. 5547841
GENERAL INFORMATION:
   STRANDEDNESS: <Unknown>
  LENGTH: 17 amino acids
   APPLICANT: Marotta, Charles A. APPLICANT: Zain, Sayeeda
  INFORMATION FOR SEQ ID NO: 240: SEQUENCE CHARACTERISTICS:
   36.4%;
55.6%;
  Query Match
Best Local Similarity 55.00,
   TYPE: amino acid
   15
  3 RLQAYLKPH 11
   7 QLGLYLSPH
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Gaps

```
TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
   US-09-239-043D-1855
; Sequence 1855, Application US/09239043D
; Patent No. 6689363
   APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
   Vitiello, Maria
   Query Match
Best Local Similarity 50.0°
  8 LGLYLSPH 15
   ||::|:|
LGIHLNPN 8
      US-09-239-043D-1855
   RESULT 14
US-08-159-339A-458
                            셤
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  셤
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   ; OTHER INFORMATION: Amino acid sequence encoding MOT isolated from potato.
US-09-463-239-29
  Gaps
   ö
   Sequence 29, Application US/09463239
; Sequence 29, Application US/09463239
; Fatent No. 6700039
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Sonnewald, Uwe
; TITLE OF INVENTION: Genetic Method for Controlling Sprouting
; FILE REFERENCE: 109846.178
; CURRENT APPLICATION NUMBER: US/09/463,239
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 9713318.0
; PRIOR FILING DATE: 1998-07-10
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
      Genetic Sequences Coding For Alzheimer
Amyloid From Brain
   DB 1; Length 20;
83;
   3; Indels
   Query Match 35.1%; Score 27; DB 4; Length 7; Best Local Similarity 85.7%; Pred. No. 3.8e+05; Matches 6; Conservative 0; Mismatches 1; Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,893
FILING DATE: 19921215
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0932.0250003
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: Genetic Sequences Coding For TITLE OF INVENTION: Amyloid From Brain NUMBER OF SEQUENCES: 18 CORRESSENDENCE ADDRESSE Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Avenue CITY: Washington STATE: D.C. COUNTRY: U.S.A.
   Score 28; DB 1
Pred. No. 83;
4; Mismatches
   TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
   ORGANISM: Artificial Sequence
   36.4%;
   20 amino acids
  5; Conservative
  |: ||||:::
| LNREEFOLGIFV 16
  1 LDSLSFQLGLYL 12
   ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
  Query Match
Best Local Similarity
Matches 5; Conserv
  -09-463-239-29
   US-07-990-893-9
  SEQ ID NO 29
LENGTH: 7
  ð
  a
```

```
APPLICANT: Livingston, Farian D.
APPLICANT: Celis, Esteban
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Edimmune Inc.
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US/09/239,043D
PRIOR FILING DATE: 1997-03-12
PRIOR PELICATION NUMBER: US/06/013,363
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US/06/013,363
PRIOR PILING DATE: 1994-03-13
PRIOR PILING DATE: 1994-11-23
PRIOR PILING DATE: 1994-11-23
PRIOR PILING DATE: 1994-11-23
PRIOR PILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US/08/205,713
PRIOR PILING DATE: 1994-07-21
PRIOR PILING D
   ö
   Gaps
  ö
  0; Indels
  35.1%; Score 27; DB 4; Length 9; 50.0%; Pred. No. 3.8e+05; tive 4; Mismatches 0; Indels
  Sequence 458, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
  TITLE OF INVENTION:
```

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Search completed: November 14, 2004, 12:08:51 Job time : 12.8085 secs
   8 LGLYLSPH 15
   ||::|:|
2 LGIHLNPN 9
   ò
   g
  APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitallo, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Chesnut, Robert
APPLICANT: Epimmune Inc.
ITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
ITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
ITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
ITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
ITLE REPERENCE: 2060.0060007
CURRENT APPLICATION NUMBER: US/09/219,043D
CURRENT FILING DATE: 1999-01-27
PRIOR RELING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
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   Gaps
   ö
   DB 3; Length 10;
   Indels
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
STATE: San Francisco
STATE: USA
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: BM Compatible COMPUTER: IBM Compatible COMPUTER: IBM Compatible COPERATING SYSTEM: DOS SOFTWARE: FastESEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 004/159,339A FILING DATE: 29-NOV-1993 CLASSIFICATION DATA:
APPLICATION NUMBER: US 004/27,746 FILING DATE: 07-AUG-1992 APPLICATION NUMBER: US 08/027,746 FILING DATE: 05-MAR-1993 APPLICATION NUMBER: US 08/103,396 FILING DATE: 06-AUG-1993 APPLICATION NUMBER: US 08/103,396 FILING DATE: 06-AUG-1993 APPLICATION NUMBER: 32,762 REGISTRATION NUMBER: 32,762 REGISTRATION NUMBER: 32,762 REFERENCE/DOCKET NUMBER: 018623-005030US TELECOMMUTCATION INFORMATION: TELECOMMUTCATION: TELECOMMUTCA
   Score 27;
   Sequence 620, Application US/09239043D Patent No. 6689363 GENERAL INFORMATION:
   35.1%;
50.0%;
  APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
   Query Match
Best Local Similarity 50.0
Matches 4; Conservative
  single
  MOLECULE TYPE: peptide
  8 LGLYLSPH 15
  ||::|:|:
2 LGIHLNPN 9
  TYPE: amino acid
STRANDEDNESS: si
  TOPOLOGY: linear
   US-08-159-339A-458
   US-09-239-043D-620
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PRIOR FILING DATE: 1997-11-25
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PRIOR PILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-13
PRIOR PLICATION NUMBER: US 60/013,363
PRIOR PLICATION NUMBER: US 60/013,363
PRIOR PLICATION NUMBER: US 08/447,610
PRIOR FILING DATE: 1995-06-05
PRIOR PLING DATE: 1994-11-20
PRIOR PLING DATE: 1994-11-20
PRIOR PLING DATE: 1994-11-21
PRIOR PLING DATE: 1994-07-21
PRIOR PLING DATE: 1994-07-21
PRIOR PLING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-03-16
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-03-16
   Gaps
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  ; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-620
   DB 4;
55;
  Mismatches
   Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
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  unidentified 5.7/3
Ig H chain V-D-J r
cystathionine gamm
  hypothetical pepticall surface adhes hypothetical prote hypothetical prote beta-fructofuranos
  tyrosine 3-monooxy
tyrosine 3-monooxy
Ig heavy chain CRD
estrogen receptor
   polygalacturonase
proton-translocati
D-SP2.5 region - m
   T-cell receptor be
T-cell receptor be
phosphoenolpyruvat
   Ig heavy chain CRD corazonin - Americ
   T-cell receptor be
  receptor be
   hypothetical prote
glucuronosyltransf
  tyrosine 3-monooxy
tyrosine 3-monooxy
  tyrosine 3-monooxy
   tyrosine 3-monooxy
   phospholipase A2
T-cell receptor b
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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   PQ0731
PH1602
PH1602
PT0586
D61440
D61440
PT0510
PT
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   US-09-831-253F-3
63
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2: pir2: *
3: pir3: *
4: pir4: *
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Sequence:
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  Searched:
  Database
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p00731

Unidentified 5.7/35K protein [imported] - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: P00731

R;Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
  PHIGOZ

IG H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PHIGOZ

Exp. Med: 178, 317-329, 1993

A;Title: Modecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PHISBO; MUID:93301609; PMID:8315387
  ö
  ö
                        T-cell receptor be alcohol dehydrogen T-cell receptor be globulin IV alpha neuromodulatory pe T-cell receptor be T-cell receptor ga probable trpEG lea alcohol dehydrogen ThR protein - Pee T-cell receptor ga T-cell receptor ga
  gene HEXA protein
6-phosphofructokin
polysialoglycoprot
sterol carrier pro
   Gaps
  Gaps
  ö
  ö
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   Query Match 38.1%; Score 24; DB 2; Length 11; Best Local Similarity 60.0%; Pred. No. 1.3e+02; Matches 0; Indels
   34.9%; Score 22; DB 2; Length 7; 50.0%; Pred. No. 2.8e+05; ive 2; Mismatches 1; Indels
  A;Experimental source: bone marrow pre-B lymphocyte C;Keywords: immunoglobulin
   ALIGNMENTS
PQ0776
PT0624
S06195
PT0624
S00066
S33246
PT0988
CP1098
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Best Local Similarity 50.0
Matches 3; Conservative
     A,Accession: PQ0731
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-11 <KOM>
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ATVVW 5
     5 ATMIW 9
  A; Residues: 1-7 < LEV>
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   A; Accession: PH1602
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proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C;Species: Rhodospirillum rubrum
C;Species: Rhodospirillum rubrum
C;Species: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C;Accession. 369123
R;Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Bur. J. Biochem. 228, 719-726, 1995
A;Title: Properties of the soluble polypeptide of the proton-translocating transhydroge: A;Reference number: 869123; MUID:95255277; PMID:7737169
  C,Accession: I49808
R;Kurosawa, Y.; Tonegawa, S.
Lsyp. Med. 155, 201-218, 1982
A;Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity A;Reference number: 149808; MUID:82099938; PMID:6798155
A;Accession: I49808
   T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: J7-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PTG519
R;Feeney, A.J
T, M.J. 115-124, 1991
A;Fille: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
  ö
  ö
  ö
   C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 149808
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  A,Molecule type: DNA
A,Residues: 1-6 <RES>
A,Cross-references: GB:J00432; NID:g194370; PIDN:AAA37904.1; PID:g450452
C,Genetics:
A,Gene: Igh
  ö
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  ö
   Length 12;
  1; Indels
  1; Indels
  1; Indels
   27.0%; Score 17; DB 2; Length 6; 50.0%; Pred. No. 2.8e+05; ive 2; Mismatches 1; Indels
   Length 6;
   28.6%; Score 18; DB 2; I 40.0%; Pred. No. 2.1e+03;
   Score 17; DB 2; I
Pred. No. 2.8e+05;
2; Mismatches 1;
   A;Status: preliminary; translated from GB/EMBL/DDBJ
   A,Molecule type: mRNA
A,Residues: 1-6 <FEE>
A,Experimental source: adult thymus, strain BALB/C
C,Keywords: T-cell receptor
  2; Mismatches
   Query Match
Best Local Similarity 40.0%;
Matches 2; Conservative
  D-SP2.5 region - mouse (fragment)
  A, Status: translation not shown
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Matches 2; Conservative
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   A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-12 <DIG>
   Query Match
Best Local Similarity
Matches 3; Conserv
   5 ATMIWT 10
  STMVTT 6
   5 ATMIW 9
  2 ADVVW 6
   A; Accession: PT0519
   셤
   ò
   음
  ò
cystathionine gamma-synthase - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Species: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: 569159
R;Ravanel, S.; Droux, M.; Douce, R.
Arch. Biochem. Biophys. 316, 572-584, 1995
Artitle: Methionine biosynthesis in higher plants. I. Purification and characterization A;Reference number: 569159; MUID:95142682; PMID:7840669
A;Accession: 569159
A;Accession: 569159
A;Ressidues: 1-10 cRAv>
A;Cross-references: UNIPROT:Q7M1J3
C;Keywords: chloroplast
   Btr
  T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Dete: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
T;Feeney, A.J.
T;Feeney, A.J.
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Fetalus: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Restaldues: 1-7 FPEB
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor
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Cispecies: O'-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
Cispecies: O'-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
Jisterillus in District of Cispecies: Aspergillus sp. polygalacturonase: multiplicity, divergence, and Aspecansion: DG1440
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Matches 3; Conservative
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509652
hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)
C;Species Enterobacter cloacae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
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A;Viiegenthart, 0.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.
Antimicrob. Agents Chemother. 33, 1153-1159, 1989
A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant inv
  glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)
N;Alternate names: UDP-glucuronyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Uul-1992 #sequence_revision 17-Uul-1992 #text_change 07-Feb-1997
C;Accession: PX0008
R;Yokota, H.; Yuasa, A.; Sato, R.
J;Biochem. 104, 531-536, 1988
A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver
   J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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  C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
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R;Fenney, A.J.
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   9 WT 10
   A; Accession: S09652
  3 WT 4
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PX0008
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C;Species: Zea mays (maize)
C;Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 51389
R;Jiao, J.; Chollet, R.
Arch. Biochem. Biophys. 283, 300-305, 1990
A;Titler: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylas
A;Reference number: 513889; MUID:91112741; PMID:2148863
   J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Dacte: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 16-Aug-2004
C;Accession: A23169
R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.
Eur. J. Biochem. 53, 91-97, 1975
A;Title: Isolation and properties of prophospholipase A2 from ox and sheep pancreas.
A;Accession: A29169
   ö
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  T-cell receptor beta chain V-D-J region (121-3BF) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Dete: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C;Accession: PT0650 #S;Peeney, A.J.
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A,Residues: 1-12 - EDUT-
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Best Local Similarity 80.05
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   SSDAT 6
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C;Accession: 155382
R;Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 266, 10739-10745, 1933
A;Title: The two allele sequences of a common polymorphism in the promoter of the plasmi A;Reference number: 155382; MUID:93266509; PMID:8388372
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Caross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021
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A;Gene: GDB:PAII
A;Cross-references: GDB:120297; OMIM:173360
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Job time : 38 secs
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  1 WT 2
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10639, A 10660, A 10715, A

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Searched:

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Sequence 140,

Sequence 3

Sequence Sequence

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BIND TO

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MEDIUM TYPE: Rioppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRNT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
ATTORNEY/AGENT INFORMATION:
NAME: Hutbiec, Robert T.
REGISTRATION NUMBER: 36,392
  Sequence 39, Application US/10083768
Publication No. US20030158116A1
GENERAL INFORMATION:
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES ADD COMPOUNDS THAT BINI
THROMBOPOISTIN RECEPTOR
US-10-324-182-6

US-90-077-439A.13

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   GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-TO.
APPLICANT: CHEETHAM, JANET C.
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: APPLICATION NUMBER: US/10/632,388
CURRENT APPLICATION NUMBER: US/03-07-31
PRIOR APPLICATION NUMBER: US/09/428,082B
PRIOR RILING DATE: 1999-10-22
PRIOR PILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
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   Sequence 67, Application US/10609217
Publication No. US2004004188A1
GENERAL INFORMATION:
APPLICANT: EBIGS, ULRICH
APPLICANT: CHEFTRAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REPERENCE: A-527
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Pred. No. 3.5e+02;
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CURRENT FILING DATE: 2003-06-27
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PRIOR PILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
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  Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstron, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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60.0%; Pred. No. 3.5e+02;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
   ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
   41.2%; Score 33; DB 14;
60.0%; Pred. No. 3.5e+02;
REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID No: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
  NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
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US-10-083-768-216
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US-10-083-768-39
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Publication No. US20030158116A1
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
CWirla, Steven E.
Duffin, David J.
Gates, Christian
   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEG ID NO: 216:
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; Publication No. US20040077022A1
; GENERAL INFORMATION:
    APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: GIDSS, USAN WARIE
; APPLICANT: GUDSS, USAN WARIE
; APPLICANT: GUDSS, USAN WARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
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; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2000-05-03
; FRIOR PILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-10-22
; PRIOR PILING DATE: 1999-10-23
; NUMBER OF SEQ ID NOS: 1157
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; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: HOMAS CHARLES
; APPLICANT: HOMS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; TITLE OF INVENTION: MODIFIED PEPTIDES
; FILE REFERENCE: A-527
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 1998-10-22
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  Sequence 67, Application US/10645761

Sequence 67, Application US/10645761

Publication No. US20040071712A1

SERERAL INFORMATION:

APPLICANT: FILLY
APPLICANT: LIU, CHARN-FA

APPLICANT: CHEETHAM, JANET C.

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527

CURRENT APPLICATION NUMBER: US/10/645,761

CURRENT FILLING DATE: 1999-10-22

PRIOR FILING DATE: 1999-10-22

PRIOR FILING DATE: 1999-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: PATENTIN NUMBER: 60/105,371

PRIOR FILING DATE: 1999-10-23

NUMBER OF SEQ ID NOS: 1133
   APPLICANT: FEIGE, URICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHESTHAM, JAMET C.
APPLICANT: CHESTHAM, JAMET C.
APPLICANT: GONGS, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/651,723
CURRENT FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFFWARE: PATENTIN VERSION 3.1
   41.2%; Score 33; DB 15; Length 14; 60.0%; Pred. No. 3.5e+02; tive 1; Mismatches 3; Indels
   Query Match 41.2%; Score 33; DB 15; Length 14; Best Local Similarity 60.0%; Pred. No. 3.5e+02; Matches 6; Conservative 1; Mismatches 3; Indels
  ) OTHER INFORMATION: TPO-MIMETIC PEPTIDE US-10-651-723-67
   OTHER INFORMATION: TPO-MIMETIC PEPTIDE US-10-645-761-67
   Sequence 67, Application US/10651723
Publication No. US20040057953A1
GENERAL INFORMATION:
  ORGANISM: Artificial Sequence
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Best Local Similarity 60.0
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                              LOGPPYVSWL 15
  6 LOGPPYVSWL 15
  1 | | : | | | 3 LVGPSLMSWL 12
  3 LVGPSLMSWL 12
   US-10-651-723-67
  US-10-645-761-67
  SEQ ID NO 67
LENGTH: 14
   SEQ ID NO 67
LENGTH: 14
   TYPE: PRT
  TYPE: PRT
   FEATURE:
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Gaps

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Indels

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Length 6;
   Score 31; DB 15; Lengtn \sigma_i
Pred. No. 1.4e+06;
  APPLICANT: University Court of the University of Glasgow TITLE OF INVENTION: Targeting peptides FILE REFERENCE: PC/MC/JM/P1191005
CURRENT APPLICATION NUMBER: US/09/990, 832C
CURRENT FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin version 3.1
LENGTH: 12
TITLE OF INVENTION: Selective Substrates for Matrix TITLE OF INVENTION: Metalloproteinases FILE REFERENCE: P-L2 543 CURRENT APPLICATION NUMBER: US/10/243,613 CURRENT FILING DATE: 2002-09-13 PRIOR APPLICATION NUMBER: US 09/953,592 PRIOR FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 129 SOFTWARE: FastSEQ for Windows Version 4.0
  38.8%; Score 31; DB 15;
83.3%; Pred. No. 1.4e+06;
  APPLICANT: BAE, JOO-eun
APPLICANT: BAE, JOO-eun
APPLICANT: KLINGEMANN, Hans G.
TITLE OF INVENTION: IMMUNGENIC PEPTIDES
FILE REFERENCE: 047940-0128
CURRENT APPLICATION NUMBER: US/10/428, 335
CURRENT APPLICATION NUMBER: US 10/138,469
PRIOR APPLICATION NUMBER: US 10/138,469
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 179
SEQ ID NO 69
   ) OTHER INFORMATION: SYNTHETIC CONSTRUCT US-10-243-613-25
  Sequence 71, Application US/0990832C Publication No. US20030149235Al GENERAL INFORMATION:
  ; Sequence 69, Application US/10428335; Publication No. US20040009186A1; GENERAL INFORMATION:
   TYPE: PRT ORGANISM: Artificial Sequence
   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 71.4%;
  Query Match 38.8
Best Local Similarity 83.3
Matches 5; Conservative
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   ; ORGANISM: Homo sapiens
US-10-428-335-69
  9 PPYVSWL 15
   10 PYVSWL 15
  3 PPIFSWL 9
  1 PYVIWL 6
   US-09-990-832C-71
   US-10-428-335-69
  SEQ ID NO 25
   FEATURE:
   Matches
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  요
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       Gaps
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  Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
  40.0%; Score 32; DB 14; Length 14; 55.6%; Pred. No. 5e+02; tive 1; Mismatches 3; Indels
       IndelB
  CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
       ښ
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   1; Mismatches
   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
  Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
  Sequence 37, Application US/10083768 Publication No. US20030158116A1 GENERAL INFORMATION:
  US-10-243-613-25
; Sequence 25, Application US/10243613
; Publication No. US20040053823A1
; GENERAL INFORMATION:
  APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwills, Steven E.
Duffin, David J.
Gates, Christian
   NUMBER OF SEQUENCES: 232
   APPLICANT: Smith, Jeffrey W. APPLICANT: Chen, Emily I. APPLICANT: Kridel, Steven J.
   Query Match
Best Local Similarity 55.6
Matches 5; Conservative
   6; Conservative
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  3 LVGPSLMSWL 12
   7 QGPPYVSWL 15
   3 OGPTLTAWL 11
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   US-10-083-768-37
   Matches
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Gaps

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Search completed: November 14, 2004, 13:36:59 Job time: 80.6667 secs
   US-09-077-439A-13
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   Sequence 6, Application US/09760397
Patent No. US3002009781A1
Patent No. US3002009781A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Gavit, Patrick D.
TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production FILE REPERENCE: 1103/11041US01
CURRENT APPLICATION NUMBER: US/09/760,397
CURRENT FILING DATE: 2001-01-12
FRIOR APPLICATION NUMBER: 09/271,970
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
   Sequence 6, Application US/10324182
Publication No. US20030194782A1
Publication No. US20030194782A1
Publication No. US20030194782A1
APPLICANT: Better, Marc D.
APPLICANT: Gavit, Patrick D.
APPLICATION NUMBER: US/10/324,182
CURRENT FILING DATE: 2002-12-20
PRIOR PELING DATE: 1089-03-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
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  0; Gaps
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   Query Match
38.8%; Score 31; DB 10; Length 12;
Best Local Similarity 44.4%; Pred. No. 6.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels
   Score 31; DB 14; Length 15;
Pred. No. 7.6e+02;
0; Mismatches 2; Indels
   Score 31, DB 9; Length 15;
Pred. No. 7.6e+02;
0; Mismatches 2; Indels
; OTHER INFORMATION: Targeting peptide sequence US-09-990-832C-71
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71.4%;
  Query Match 38.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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  9 PPYVSWL 15
  9 PPYVSWL 15
  2 PPKVGWL 8
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US-09-760-397-6
  LENGTH: 15
TYPE: PRT
ORGANISM: Human
  9-160-391-60 SD
  US-10-324-182-6
   SEQ ID NO 6
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RESULT 15

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   Gape
  General involvation;

APPLICANT: Collier, R. John
APPLICANT: Blanke, Steven R.
APPLICANT: Banson, Ericka L.
APPLICANT: Banson, Ericka L.
APPLICANT: Banson, Mine, Jill C.
APPLICANT: Banson, Michael N.
APPLICANT: Starnbach, Michael N.
TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity
TITLE OF INVENTION: Use of Toxin Peptides into Cells
TITLE OF INVENTION: Use of Toxin Peptides into Cells
FILE REFERENCE: 00246/187002
CURRENT FILING DATE: 1995-04-08
PRIOR FILING DATE: 1995-04-08
PRIOR PLICATION NUMBER: DCT/US96/20463
PRIOR FILING DATE: 1996-06-07
PRIOR PELING DATE: 1995-12-13
PRIOR PELING DATE: 1995-12-13
PRIOR PELING DATE: 1995-12-13
PRIOR PELING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
  ö
   37.5%; Score 30; DB 10; Length 9; 66.7%; Pred. No. 1.4e+06;
   1; Indels
  1; Mismatches
; Sequence 13, Application US/09077439A
; Publication No. US20030202989A1
; GENERAL INFORMATION:
  Query Match 37.5
Best Local Similarity 66.7
Matches 4; Conservative
  ORGANISM: Mus musculus
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  Total number of hits satisfying chosen parameters:
   2002273 segs, 358729299 residues
  November 14, 2004, 12:55:26
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  BLOSUM62
Gapop 10.0 , Gapext 0.5
   1 EAVLILQGPPYVSWL 15
   US-09-831-253F-8 7
              Copyright
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seq length: 15
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  Minimum DB s
Maximum DB s
  Sequence:
   Searched:
  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\*

geneseqp2003bs:\* geneseqp2004s:\*

| Description                | Aay92952 Transform Aay93104 Transform Aaw36644 Thrombopo Aaw366767 Thrombopo Aaw17011 TPO-mimet Aau25853 Human thr Abb72897 TPO mimet Adj52689 TPO mimet Adj52689 TPO mimet Adj52689 TPO mimet Adj52684 CH1 delet Adj52684 CH2 delet Adj51644 CH2 delet Adj6184 Hepatitis Adw01381 Hepatitis Adw01381 Hepatitis Aaw83368 PspGI met Aaw36481 Thrombopo Aaw36631 Thrombopo Aaw36631 Thrombopo Aaw36631 Human thr Aaw36631 Human coa Aaw36699 Human Dep Abr55023 MMP-2 sel Adk14204 Matrix me Aaw37010 TRP-2 der Adm22859 Human CD3 Aaw25851 Synthetic |
|----------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SUMMARIES                  | AAY92952<br>AAY93104<br>AAW36634<br>AAW36634<br>AAW36767<br>AAB72893<br>AAB72893<br>AD51644<br>AD51644<br>AD51644<br>AD805646<br>AD805646<br>AAW363181<br>AAW363181<br>AAW369981<br>AAW3669<br>AAW3669<br>AAW3669<br>AAW3669<br>AAW3669<br>AAW3600000000000000000000000000000000000                                                                                                                                                                                                                                                                 |
| DB                         | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| %<br>Query<br>Match Length | 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| %<br>Query<br>Match        | 0 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Score                      | 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Result<br>No.              | 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

| Synt                         | Aar29768 PIA TRA a<br>Aar63674 Antigenic | Aar63152 PIA tumou | Aar89158 Peptide P | Aaw29251 Immunomod | Aaw22041 Antigenic | Aaw68309 MHC bindi | Aay41263 H-2Ld-res | Aay03653 P1A tummo | Aay22128 PlATRA an | Aag66423 Mouse mas | Aag78821 P815AB pe | Aau76804 MHC class | Aae35597 P1A prote | Abp58361 Mastocyto | Abr44537 PlA-1 pep | Aao23280 PIA (35-4 |
|------------------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 8 2 AAW25562<br>8 2 AAW25561 | 9 2 AAR29768<br>9 2 AAR63674             | 9 2 AAR63152       | 9 2 AAR89158       | 9 2 AAW29251       | 9 2 AAW22041       | 9 2 AAW68309       | 9 2 AAY41263       | 9 2 AAY03653       | 9 2 AAY22128       | 9 4 AAG66423       | 9 4 AAG78821       | 9 5 AAU76804       | 9 6 AAE35597       | 9 6 ABP58361       | 9 6 ABR44537       | 9 6 AAO23280       |
|                              | 30 37.5<br>30 37.5                       | 30 37.5            | 30 37.5            | m                  | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            | 30 37.5            |
| 26                           | 78<br>78                                 | 30                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\*

Database :

Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis. Transforming growth factor inhibitory peptide #8. (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA. Š AAY92952 standard; peptide; 15 98ES-00002465. 99WO-ES000375. (first entry) WO200031135-A1. Homo sapiens. 23-NOV-1999; 24-NOV-1998; 08-NOV-2000 02-JUN-2000. AAY92952; AAY92952 

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Claim 9; Page 82; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

RESULT 2

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AAY93104

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The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
  Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
  Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.
   Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates
Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
   Thrombopoietin receptor binding peptide
  Disclosure; Page 26; 106pp; English
              AAW09483 standard; protein; 14 AA.
   TPO receptors on living cells
  95US-00472371.
95US-00473604.
95US-00476168.
   96WO-US008998
  95US-00478128
95US-00484090
   95US-00485301
   41.2%;
   60.08;
  (first entry)
   11-MAR-1998 (first entry)
  6; Conservative
  (GLAX ) GLAXO GROUP LTD.
   LQGPPYVSWL 15
  LVGPSLMSWL 12
   WPI; 1997-051883/05.
   Query Match
Best Local Similarity
   Sequence 14 AA;
   WO9640189-A1
   05-JUN-1996;
  10-SEP-1997
  07-JUN-1995;
   07-JUN-1995;
07-JUN-1995;
   07-JUN-1995;
  19-DEC-1996
  07-JUN-1995
  Synthetic.
   AAW09483;
  AAW36634;
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  m
  Matches
AAW09483
  AAW36634
   RESULT
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   The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides ANY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
  Hepatotropic, antagonist, transforming growth factor betal, TGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis.
   Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
  Gape
   Gaps
  Lasarte Sagastibelza JJ, Prieto Valtuena J;
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   Length 15;
  Length 15;
  Indels
   Indels
                                 Score 80; DB 3; Len
Pred. No. 7.9e-06;
  Transforming growth factor inhibitory peptide P150.
  Score 80; DB 3; L. Pred. No. 7.9e-06; ; Mismatches 0;
   (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA
   Disclosure, Page 33; 86pp; Spanish.
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   AAY93104 standard; peptide; 15
  100.0%;
   Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
   99WO-ES000375
  98ES-00002465
  1 EAVLILOGPPYVSWL 15
  EAVLILQGPPYVSWL 15
   1 EAVLILOGPPYVSWL 15
   1 EAVLILOGPPYVSWL 15
   (first entry)
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  WPI; 2000-411935/35.
  Ezquerro Saenz IJ,
   Borras Cuesta F;
   Sequence 15 AA;
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   WO200031135-A1.
   23-NOV-1999;
  24-NOV-1998;
   08-NOV-2000
  02-JUN-2000
  AAY93104;
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Johnson SS;

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   Gaps
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   Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
Length 14;
Score 33; DB 2; Length 14;
Pred. No. 2.4e+02;
t; Mismatches 3; IndelB
   Thrombopoietin receptor binding peptide.
  AAW36634 standard; peptide; 14 AA.
```

RESULT 3

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Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
   can be
  bone
   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; oytostatic; antiaschmatic; thrombolyvic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; oytocoxic r cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
   DJ, Gates CM, Johnson SS;
Wrighton NC;
  Gaps
   The present peptide, which binds the thrombopoietin receptor (TR), consed to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and thrombopoietin dependent cell lines
   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
  ö
   Score 33; DB 2; Length 14;
Pred. No. 2.4e+02;
  3; Indels
  1; Mismatches
  TPO-mimetic peptide sequence SEQ ID NO:67.
   Dower WJ, Barret RW, Cwirla SE, Duffin
Mattheakis LC, Schatz PJ, Wagstrom CR,
  ξ
  Boone
  Example 9; Page 75; 106pp; English.
  AAB17011 standard; peptide; 14 AA.
  Liu C, Cheetham J,
95US-00478128
               95US-00485301.
   41.2%;
   99WO-US025044
  98US-0105371P
  31-OCT-2000 (first entry)
  6; Conservative
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  3 LVGPSLMSWL 12
   WPI; 2000-350702/30.
  WPI; 1997-052226/05.
   6 LQGPPYVSWL
   Query Match
Best Local Similarity
   (AMGE-) AMGEN INC.
   Sequence 14 AA;
   WO200024782-A2
07-JUN-1995;
07-JUN-1995;
   25-OCT-1999;
  23-OCT-1998;
22-OCT-1999;
  04-MAY-2000.
  Synthetic.
   AAB17011;
  Feige U,
  Matches
   RESULT 6
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  ö
  The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
  Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
  Gaps
  Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor – useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
  ö
   Thrombopoietin receptor; binding peptide; treatment; agonist; haemacological disorder; thrombocytopaenia; chemcherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
   Length 14;
   41.2%; Score 33; DB 2; Length 14; 60.0%; Pred. No. 2.4e+02; tive 1; Mismatches 3; Indels
  Thrombopoietin receptor binding peptide.
  Disclosure; Page 26; 106pp; English.
  Location/Qualifiers
  AAW36767 standard; peptide; 14 AA
   /note= "NH2-Cys"
   96WO-US009623.
  95US-00478128
95US-00485301
   96WO-US009623
   (first entry)
   Local Similarity 60.0
nes 6; Conservative
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  3 LVGPSLMSWL 12
   WPI; 1997-052226/05.
  Sequence 14 AA;
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   07-JUN-1996;
  WO9640750-A1
  WO9640750-A1
   07-JUN-1996;
   07-JUN-1995;
  07-JUN-1995;
   11-MAR-1998
   19-DEC-1996
  19-DEC-1996
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   Synthetic.
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   Query Match
  Matches
   AAW36767
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WPI; 2002-130313/17.
  Matches
   RESULT 8
  ABB72897
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   The present invention describes composition of matter (1) comprising an FC domain, pharmacologically active peptides, and linkers. Where (1) is: (X1)5-P1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(I1)C-P1-(I2)G-P2, -(I1)C-P1-(I2)G-P2, -(I1)C-P1-(I2)G-P2-(I3)E-P3, or -(I1)C-P1-(I2)G-P3-(I4)F-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; IJ, IZ, IJ, and IA = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or I, provided that at least 1 of a and b is I. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Pab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and cossibly placental transfer. AAA69413 to AAA69526 and AAB16955 to exemplification of the present invention
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   Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
   Podduturi S;
  Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells
  Gaps
  ö
   Human thrombopoietin receptor (TPO-R) activator peptide #39.
  Schatz PJ;
Deprince RB,
   41.2%; Score 33; DB 3; Length 14; 60.0%; Pred. No. 2.4e+02;
  3; Indels
  Dower WJ, Barrett RW, Cwirla SE, Gates CM,
Balasubramanian P, Wagstrom CR, Hendren RW,
  1; Mismatches
          Claim 19; Page 217; 608pp; English
  AAU25853 standard; peptide; 14 AA.
   95US-00478128.
95US-00485301.
96WO-US009623.
  01-MAR-2000; 2000US-00516704.
  96US-00699027
   (first entry)
   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
  (GLAX ) GLAXO GROUP LTD.
  6 LOGPPYVSWL 15
   3 LVGPSLMSWL 12
   WPI; 2001-564142/63.
  Sequence 14 AA;
  Homo sapiens.
   US6251864-B1.
   07-JUN-1995;
  107-JUN-1995;
  15-AUG-1996;
  17-DEC-2001
   26-JUN-2001
   AAU25853;
   rin 0;
   RESULT 7
  AAU25853
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
bind to and activate the human thrombopoletin receptor (TPD-R). Methods
of activating thrombopoletin receptors in cells comprise contacting the
cells with effective amounts of peptides and peptide mimetics attached to
cells with effective amounts of peptides and peptide mimetics attached to
chydrophilic polymers. The methods are used to treat thrombocytopenia auch
contacting the confemcifieraby, radiation therapy or bone-marrow
cransplantation and to prevent thrombocytopenia in patients at isk. The
sequences are used to treat and prevent haematological disorders
confluing thrombocytopenia and platelat disorders in vitro
as unique tools for understanding the biological role of thrombopoietin
consumption of develop other compounds that bind to and activate the TPO
ceeptor. The peptides can be used to detect TPO receptors on living
cells and fixed cells, in biological fluids, in tissue homogenates, and
consumption of mutural biological materials. They may also be used for in
situ staining, fluorescence-activated cell sorting, western blotting and
consume.linked immunosorbent assay (ELISA). In addition, the peptides can
be used for in vitro expansion of megakarycytes and their committed
consumptical alone or in conjunction with additional cytokines
  ö
   erythropoletin; Then the cross factor alpha inhibitor; The cross of the control of the cross of 
   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; 1gG; EPO;
  Gaps
with peptides and peptide mimetics attached to hydrophilic polymers
  ö
  Length 14;
  Score 33; DB 4; Length 14;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
   Gudas JM;
   Boone TC,
   Disclosure; Col 20; 128pp; English
   Š
   TPO mimetic peptide SEQ ID NO:67.
   ABB72897 standard; peptide; 14
   Feige U, Liu C, Cheetham JC,
   41.2%;
60.0%;
   02-MAY-2001; 2001WO-US014310.
  03-MAY-2000; 2000US-00563286
  05-APR-2002 (first entry)
  Conservative
   | || :|||
LVGPSLMSWL 12
  6 LQGPPYVSWL 15
  Fanconi's syndrome.
  Local Similarity
  (AMGE-) AMGEN INC.
   Sequence 14 AA;
  WO200183525-A2
   Homo sapiens.
   08-NOV-2001.
  9
  Synthetic
   ABB72897;
   Query Match
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The present invention describes a ventice-peptice molecule (1) or its multimers. (1) can have autiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antianthritic, antidiabetic, ophthalmological and anterpretetive activities. (1) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (1) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (1) is useful for treating inflammatory and autoimmune diseases, unmour growth, cancer, returnating inflammatory and autoimmune diseases. (1), comprising confertility, and neurological degenerative diseases. (1), comprising compounds are useful for treating disorders characterised by low mimetic compounds are useful for treating disorders characterised by compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet compounds are useful in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABBJ5695 to ABBJ5777 exprement amino acid and nucleic acid sequences used in the
  mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
   present invention describes a vehicle-peptide molecule (I) or its
              Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
  ö
  41.2%; Score 33; DB 5; Length 14; 60.0%; Pred. No. 2.4e+02;
  Ghrayeb J;
  1; Mismatches
   exemplification of the present invention
   TPO mimetic peptide sequence SeqID 502
   Scallon BJ,
  Claim 39; Page 44; 176pp; English
  ADJ73048 standard; peptide; 14 AA.
  24-MAR-2003; 2003WO-US009139
   29-MAR-2002; 2002US-0368791P
   (first entry)
  6; Conservative
   Heavner GA, Knight DM,
   6 LQGPPYVSWL 15
   LVGPSLMSWL 12
   (CENZ ) CENTOCOR INC.
  WPI; 2003-804237/75.
  Query Match
Best Local Similarity
   WO2003084477-A2.
  Sequence 14 AA;
   06-MAY-2004
  16-OCT-2003.
   Synthetic.
   ADJ73048;
  Matches
  RESULT 9
  ADJ73048
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This invention relates to novel mammalian CDR mimetibodies, specific fragment where a protein has been inserted into, or replaces a portion of fragment where a protein has been inserted into, or replaces a portion of of one or more CDR regions, such that each CDR mimetibody comprises at least one human framework region and at least one itself comprises at least one human framework region and at least one ligand binding region (LDR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modilating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a mimetibody of the invention.
   New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
  Gaps
variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
   CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
  hypotensive; neuroprotective; noctropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
  ö
  Nesspor TC;
   Score 33; DB 7; Length 14;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
  Ghrayeb J, Scallon BJ,
   CH1 deleted mimetibody-related peptide SegID502.
  Disclosure; SEQ ID NO 502; 97pp; English.
   ADJ52683 standard; peptide; 14 AA.
   viral infection; fungal infection
   41.2%;
   27-JUN-2003; 2003WO-US020347
   28-JUN-2002; 2002US-0392431P
  60.08;
  (first entry)
  6; Conservative
  Knight DM,
  | || :|||
LVGPSLMSWL 12
   6 LQGPPYVSWL 15
   (CENZ ) CENTOCOR INC
  WPI; 2004-082870/08.
   Best Local Similarity
  WO2004002417-A2.
   Sequence 14 AA;
  Kutoloski KA;
  Unidentified
  06-MAY-2004
  08-JAN-2004.
  Heavner GA,
  Synthetic
  ADJ52683;
   Query Match
  Matches
   RESULT 10
  ADJ52683
       à
   셤
   Property of the contract of th
   ö
   Gaps
  New CDR mimetibody comprising a portion of a heavy or light chain
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WPI; 2004-082872/08.
   ABB05646;
  Query Match
  RESULT 12
  ABB05646
    8
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   which encode them), compositions, methods and uses. The invention may useful for the development of compounds with an immunosuppressive, cardiavascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucida or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for disposing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example multiple sclerosis, dementia failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease or disorders, anaemia, cancerous conditions, or infectious diseases for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
  This invention relates to CH1 deleted mimetibodies (and the DNA sequences
  dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gastrointestinal-Gen; gaptraecological-Gen; heatotrointestinal-interment of immunomodulator; antiallergic; muscular-Gen; cytostatic; antialflammatory; neuroleptic; ophthalmological; mephrotropic; respiratory-Gen; tummour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dental disorder; ear disorder; nose disorder; edental disorder; disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; allergic disorder; edental disorder; edental disorder; edental disorder; disorder; metalogical disorder; metalogical disorder; metalogical disorder; edental edental disorder; edental edental disorder; edental ed
   Gaps
   ;
  Nesspor TC;
   41.2%; Score 33; DB 8; Length 14; 60.0%; Pred. No. 2.40+02; ive 1; Mismatches 3; Indels
  Ghrayeb J, Scallon BJ,
   CH1 deleted mimetibody-related peptide SegID502.
  Claim 2; SEQ ID NO 502; 129pp; English.
   renal disorder; pulmonary disorder
  ADJ51644 standard; peptide; 14 AA.
   28-JUN-2002; 2002US-0392431P.
  10-JUN-2003; 2003WO-US020495
   (first entry)
  Best Local Similarity 60.0
Matches 6, Conservative
  Knight DM,
   6 LQGPPYVSWL 15
  1 | | :|||
3 LVGPSLMSWL 12
  (CENZ ) CENTOCOR INC.
  WO2004002424-A2.
  Sequence 14 AA;
  Heavner GA, 1
Kutoloski KA;
   Unidentified,
   06-MAY-2004
  08-JAN-2004
  Synthetic
   ADJ51644;
  Query Match
ò
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This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, muditory, endocrine-Gen, gynaecological-Gen, hepatotropic, haemostatic, cardiovascular-Gen, gynaecological-Gen, hepatotropic, haemostatic, antiinflammacory, neuroleptic, opthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-condulator or cytokine-agonist. The methods and compositions of the present invention are useful for the disposical, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermandological, ear, nose or throat, endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infections, constitution and orange and orange and ophibalmologic, musculoskeletal, oncological, neutritional, ophibalmologic, masculoskeletal, oncological, neutritional, ophibalmologic, endocrine, and or peptide which may be used during the creation of a
  ö
   Novel human thyroglobulin 38 and polynucleotide for coding this polypeptide, useful for treating diseases such as simple goiter, thyroiditis, hyperthyroidism, hypothyroidism, thyroid tumor and nodular
   Human, thyroglobulin 38; cytostatic; antiinflammatory, simple goitre;
thyroiditis; hyperthyroidism; hypothyroidism; thyroid tumour;
  Gaps
New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and nutritional disorders.
  ö
   Human thyroglobulin 38 protein N-terminal peptide SEQ ID NO:7.
   Length 14;
   Score 33; DB 8; Length 14;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
  Claim 15; SEQ ID NO 502; 123pp; English.
  (BODE-) BODE GENE DEV CO LTD SHANGHAI.
  ż
  ABB05646 standard; peptide; 15
   41.2%;
  29-APR-2000; 2000CN-00115532.
  29-APR-2000; 2000CN-00115532.
   mimetibody of the invention.
   29-APR-2002 (first entry)
   Local Similarity 60.0
  6 LOGPPYVSWL 15
  3 LVGPSLMSWL 12
  WPI; 2002-140635/19.
  Sequence 14 AA;
   nodular goitre.
  Mao Y, Xie Y;
   Homo sapiens
   CN1321665-A.
  14-NOV-2001.
  THE STANDARD ```

Gaps

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Example goiter.

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This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antiganic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a hepatitis C virus CTL epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                               pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; epitope peptide; HLA-allele; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 8; Length 10;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
  Score 32; DB 8; Length 9; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus CTL epitope peptide #1014.
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 70; 220pp; English.
                                                                                                                                                                                                                                              ADK03184 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW83368 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Habel A;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2003; 2003WO-EP008112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-2002; 2002AT-00001124
11-JUL-2003; 2003EP-00450171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                               (first entry)
                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattner F, Schmidt W,
                                                                                        7 QGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 QGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QOPPLVWWL 10
                                                                                                                                 QOPPLVWWL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INTE-) INTERCELL AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-169243/16.
                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004011650-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                      ADK03184;
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    Query Match
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                                                                                                                                                                                                RESULT 14
ADK03184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW83368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigachic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present
                                                                                 The present invention describes human thyroglobulin 38 protein (I). (I) and has cytostatic and antilinflammatory activities. (I) and the polynucleotide (II) encoding it can be used in the treatment of diseases such as simple goitre, thyroiditis, hyperthyroidism, hypothyroidism, thyroid tumour and nodular goitre. The present sequence represents the N-terminal peptide of human thyroglobulin 38, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; epitope peptide; HLA-allele; CTL.
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                         41.2%; Score 33; DB 5; Length 15; 45.5%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                           5; Page 18 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus CTL epitope peptide #1011.
                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 70; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK03181 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2003, 2003WO-EP008112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2002; 2002AT-00001124.
11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                             4 LILOGPPYVSW 14
                                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-169243/16.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004011650-A2.
                                                                                                                                                                                                                                                                Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
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ADK03181;

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Gaps

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A Mary Services

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The present invention describes a type II restriction endonuclease, designated PspGI, from Pyrococcus species G-I-H. The endonuclease recognises and cleaves the following base sequence before the first C at the 5' end, to give a five base overhang at the 5' end; 5'-CC(A/T)GG-3'. Also described are: (1) isolated DNA (1) obtainable from Pyrococcus species G-I-H and coding for the PspGI restriction endonuclease; (2) isolated DNA (II) obtainable from ATCC No. 98435 and coding for the PspGI restriction endonuclease; (2) isolated DNA (II) obtainable from ATCC No. 98435 and coding for the PspGI cestriction endonuclease and methylase; (3) a recombinant DNA vector into which (1) is inserted; (4) a cloning vector comprising (II); and (5) a chart cell transformed with the vector as in (3) or (4). The endonuclease can be isolated using conventional protein purification techniques from Pyrococcus sp. G-I-H. Alternatively, the endonuclease, along with its corresponding methylase can be obtained using recombinant DNA techniques. Restriction endonuclease PspGI is useful in genetic engineering. The DNA, vectors and host cells are all useful for recombinantly producing the endonuclease in commercial quantities. The present sequence represents motif IV from the PspGI methylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Type II restriction endonuclease from Pyrococcus species G-I-H - and DNA coding for the endonuclease, optionally with its methylase for recombinant production of the restriction enzyme.
                                                                                                          PspGI; type II restriction endonuclease; Pyrococcus; methylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

40.0%; Score 32; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
                                                               PspGI methylase motif IV peptide.
                                                                                                                                                                                                                                                                                                                                                                                           (NEWE ) NEW ENGLAND BIOLABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example, Page 32, 47pp, English.
                                                                                                                                                                                                                                                                                                         98WO-US006332
                                                                                                                                                                                                                                                                                                                                                    97US-00856663
                      11-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Morgan RD, Chang Z;
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                                                                                                                                                                          Pyrococcus sp.
                                                                                                                                                                                                                   WO9851783-A1.
                                                                                                                                                                                                                                                                                                       31-MAR-1998;
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                                                                                                                                 recombinant.
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Gaps . 0

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Search completed: November 14, 2004, 13:11:17 Job time: 95.3333 sec8

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Q8g119 borrelia bu
Q8g124 borrelia bu
O61340 panulirus i
P03053 escherichia
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O9rq22 salmonella
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                                                                                                                                                November 14, 2004, 12:56:07; Search time 100 Seconds (without alignments) 86.306 Million cell updates/sec
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P83647
P80735
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                        1825181 segs, 575374646 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 15
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Maximum DB seq
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Perfect score:
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Eukaryota, Rhodophyta, Florideophyceae, Gracilariales, Gracilariaceae,
Gracilariopsis.
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Bukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
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        P21140
P21141
P19990
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P82687
P82689
Q99193
Q772h89
Q6000
Q6000
Q71zx62
P34938
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Pred. No. 3.9e+02;
1; Mismatches 1; Indels
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U59764; AAB17950.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.

NON_TER
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Lang B.Franz., Goff L.J., Gray M.W.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, US97631, ABB17951.1, -.
GO, GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0831666D0E8C65B0 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                     13 AA
                                                                                                                                                                                         ALIGNMENTS
       LCK1_LEUMA
LCK2_LEUMA
LCK8_LEUMA
PK1_PERAM
PK3_PERAM
Q99193
Q7PES9
Q7MES0
Q7MES0
Q7LZCS
Q7LZCS
Q7LZCS
UE1S_HORVU
                                                                                                                                                                                                                                                                                                             Cytochrome oxidase subunit 3 (Fragment) Name=cox3;
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Name=cox3;
                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%;
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                    PRELIMINARY;
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
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01-FEB-1997
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Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;

"[Hyp3]Met-callatostatin. Identification and biological properties of
a novel neuropepitide from the blowfly Calliphora vomitoria.";
a novel neuropepitide from the blowfly Calliphora vomitoria.";

"I Biol. Chem. 269:210659-21066(1994)

"I Biol. Chem. 269:210659-21066(1994)

"I biol. Chem. 269:21066(1994)

"I create in the integration of information within the brain. May be involved in the control of visceral muscles due to its ability to behave as potent inhibitors of peristalic movements. May also tulfill a neurohormonal role on muscles of the gut and heart.

"I ISSUE SPECIFICITY: Neurons within brain and abdominal ganglion."

"I SIMILARITY: Belongs to the allactostatin family.

PIR, E47393; E47393.

"MoD RES B Hydroxylation; Neuropeptide.

"MoD RES B Hydroxyproline (partial).

"MOD RES B Hydroxyproline amide.

"SEQÜENCE B AA; 883 MW; 7D9879CABB477768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (Rel. 44, Last annotation update)
Probable profilin LP04 (Fragments).
Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.8%; Score 27; DB 1; Length 13; 44.4%; Pred. No. 1.8e+03; ive 3; Mismatches 2; Indels
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PROSITE; PS00414; PROFILIN; PARTIAL.
Actin-binding; Cytoskeleton; Direct protein sequencing;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0A3022EE0E52C68B CRC64;
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PROX CRYSA
ID PROX CRYSA
STANDARD; PRT; 13 AA.
AC PB04647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 44, Last sequence update)
DF 10-OCT-2004 (Rel. 44, Last sequence update)
DF 10-OCT-2004 (Rel. 44, Last sequence update)
DF 10-OCT-2003 (Rel. 44, Last sequence update)
DF 10-OCT-2003 (Rel. 44, Last sequence update)
DF 10-OCT-2003 (Rel. 47, Last sequence update)
RT SEQUENCE.
RA HOSESINI Salakdeh S.G., Bennett J.;
RT "Proteome analysis of rice panicle.";
RA HOSESINI Salak to actin and affects the structor of concentrations By binding to PIP2, it inhibition of concentrations By binding to PIP2, it inhibition of Superior Super
                              MEDLINE=94342269; PubMed=8063725;
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Best Local Similarity 100...
'... 4; Conservative
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S AYMVIQGEP 13
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P41841;
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 44, Last annotation update)
Callactostatin 5 (Met-callacostatin 1) ([Hyp3]Met-callatostatin).
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Calliphora.
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Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20483622; PubMed=11027583; DOI=10.1006/bbrc.2000.3595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 1; Length 13; Pred. No. 1.2e+03;
                                                     36.2%; Score 29; DB 2; Length 13; 42.9%; Pred. No. 8.5e+02;
                                                                                                          1; Indels
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13 AA; 1565 MW; 305BD4028745B043 CRC64;
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MOD RES 13 13 Tyrosine amide.

SEQUENCE 13 AA, 1503 MW, 483D5C7E34C72727 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       13 AA.
                                                                                                          3; Mismatches
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                                                                           Local Similarity 42.5
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                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Lamiales, Lamiaceae, Lamioideae, Leonurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graus-Goeldner A., Graus H., Schlacher T., Hoegenauer G.;
"The sequences of genes bordering oriT in the enterotoxin plasmid
P307: Comparison with the sequences of plasmids F and R1.";
Plasmid 24:119-131(1990).
EMBL; MG2966; AAA25525-1;
PINF, E37390; E37390.
GO, GO:0005766; C:extracellular; IEA.
GO, GO:000746; P:conjugation; IEA.
InterPro; IPR088973; TraA.
Plasmid.
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Chem. Pharm. Bull. 39:712-715(1991).
PIR; JU0356; JU0356.
SEQUENCE 12 AA; 1354 MW; 300727313BC1B768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91100597; PubMed=2070452;
Kinoshita K., Tanaka J., Kuroda K., Koyama K., Natori S.,
Kinoshita T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.7%; Score 23; DB 2; Length 12; 80.0%; Pred. No. 7.9e+03; tive 0; Mismatches 1; Indels
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                                                                                                                                                                              01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                                                                                                                                                  12 AA
Mismatches
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                                 2 AVLILQGPPY 11
                                                                1 ATYTLPEPPY 10
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                                                                                                                                                                                                                                  Cycloleonurinin
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Plasmid P307.
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MEDLINE=85140235; PubMed=2858095;
Nordstrom J.L., Hall S.L., Kessler M.M.;
"Polyadenylylation of sea urchin histone RNA sequences in transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pfam; PF00081; Sod Fe N; 1.
PROSITE; PS00088; SOD-MN; PARTIAL.
Direct protein sequencing; Iron; Metal-binding; Oxidoreductase; Zinc.
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STRAIN=KCTC 9006;
MEDLINE=97056064; PubMed=8900409;
Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
Histone H2A (Fragment).
Psammechinus miliaris (Sand sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinoidea;
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Streptomycineae; Streptomycetaceae; Streptomyces.
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01-NOV-1997 (Rel. 35, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                   -<1 9 histone H2A.
14 AA; 1620 MW; 298A3F878A462268 CRC64;
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                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 82:1094-1098(1985)
EMBL; M12542; AAA30028.1; -.
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Pred. No. 6.8e+03;
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                             PRELIMINARY;
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Best Local Similarity
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FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS
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                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Calotropia I (EC 34.22.) (Fragment)
Calotropia gigantea (Wadar) (Bowatring hemp)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; edicotyledons; core eudicots; asterids; lamiids; Gentianales; Apocynaceae; Asclepiadoideae; Asclepiadeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishimura M., Matsuo H., Sugiyama M.; "Blasticidin S-producing Streptomyces morookaensis possesses an enzyme activity with hydrolyzes puromycin."; FEMS Microbiol. Lett. 132:95-100(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                         Bhattacharya D., Sengupta A., Sinha N.K.;
"Chemical modification and amino terminal sequence of calctropin DI
"Chemical modification and amino terminal sequence of calctropin glantea.",
Phytochemistry 26:633-63:6(1987).
-!- SIMILARITY: Belongs to peptidase family C1.
MEROPS; C01.011; -.
                                                                                                                                                                                                                                                                                                                        InterPro, IPR000169, Pept_cys_acsite.
PROSITE, PS00640; THIOL_PROTEASE_ASN; PARTIAL.
PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
Direct protein sequencing; Hydrolase; Pyrrolidone carboxylic acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1970;
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PubMed=9538199;
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Local Similarity 50.0%;
Les 4; Conservative (
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14 AA; 1715 MW;
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2 DAILSVQG 9
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SEQUENCE
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P81801;
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                                                                  CALGI
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Matches
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P81801
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01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
05-MITCHERBLEAL 27, Last annotation update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Borrelia burgdorferi plasmid cp32-7, possible partition proteins, complete cds (Borrelia burgdorferi plasmid cp32-6, possible partition proteins, complete cds) (Fragment).

Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                     FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.

BIXTME REGULATION: STIMULAFED BY DIT. STRONGLY INHIBITED BY ZINC
ION, FERROUS ION, CUPRIC ION, N-BRCHUX ION, N-BROWOSUCCINIMIDE AND
N-ETHYEMALEIMIDE. PARTIALLY INHIBITED BY COBALT ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY_2000 (TrEMBLrel. 13, Last sequence update)
01-MAY_2000 (TrEMBLrel. 13, Last annotation update)
Light-harvesting antenna of photosystem I 730, LHCI 730.
Hordeum vulgare (Barley)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knoetzel J., Svendsen I., Simpson D.J.; "Identification of the photosystem I antenna polypeptides in barley. Isolation of three pigment-binding antenna complexes."; Eur. J. Blochem. 206:209-215(1992).
Q
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Plasmid cp32-7, and Plasmid cp32-6.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                             THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-WETHYL-L-
TYROSINE MOIETIES. THE OPTIMUM PH IS 0.0 AND THE OPTIMAL
TEMPERATURE IS 45 DEGREES CELSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AA; 1588 MW; 3975624AFD65202D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          3F980730E45EF3D8 CRC64;
                                                                                                                                                                                                                                               -!- SUBUNIT: MONOMER.
-!- MISCELLANBOUS: HAS AN ISOELECTRIC POINT OF 6.4.
GO; GO:0004177; F:aminopeptidase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
Minopeptidase; Hydrolase.
NON TER
SEQÜENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 2; I
Pred. No. 9.3e+03;
1; Mismatches 1;
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Pred. No. 1e+04;
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STRAIN=B31; PLASMID=cp32-7, and cp32-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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60.0%;
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57.1%;
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STRAIR=Sh-2-82;
MEDLINE=229054;
MAILLE J.C.;
Stevenson B., Miller J.C.;
"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
Mol. Evol. 57:309-324 (2003).
EMBL; AX142090; AAN17861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Angiotensin-converting enzyme inhibitor.
Thunnus albacares (Yellowfin tuna) (Nechunnus macropterus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                       Gaps
            Stevenson B., Cabjens S., Rosa P.;
"Evidence of past recombination events among the genes encoding the Ery antigens of Borrella burgdorferi.";
Microbiology 144:1869-1879(1998).
EMBL, AF022483; AAC35454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid group cp32-3.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                       ;
                                                                                                                                                        Score 22.5; DB 2; Length 13;
Pred. No. 1e+04;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.1%; Score 22.5; DB 2; Length 15; 44.4%; Pred. No. 1.2e+04; tive 2; Mismatches 2; Indel8
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SEQÜENCE 15 AA; 1777 MW; 4E441D04EF501763 CRC64;
                                                                                                             NON_TER 1 1 1 SEQUENCE 13 AA; 1551 MW; 4E441D04EF054373 CRC64;
                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel: 23, Created)
01-MAR-2003 (TrEMBLrel: 23, Last sequence update)
01-UNN-2003 (TrEMBLrel: 24, Last annotation update)
PF-50 proctein (Fragment).
Name=PF-50;
                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                      15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Muscle;
MEDLINE=88326322; PubMed=3415688;
MEDLINE=98361033; PubMed=9695920;
                                                                                                                                                      Query Match 28.1%;
Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4.,
4; Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 QGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 QG-PLIKWI 10
                                                                                                                                                                                                                  7 QGPPYVSWL 15
                                                                                                                                                                                                                                   1 QG-PLIKWI 8
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P18691;
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RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;

RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle.";

RL Biochem. Biophys. Res. Commun. 155:332-337(1988).

CC -!- FUNCTION: Inhibits angiotensin-converting enzyme.

DR PIRT A31570.

CK -!- FUNCTION: Inhibits angiotensin-converting enzyme.

SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Chery Match

Best Local Similarity 33.34; Pred. No. 1.88+06;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps

CY 9 PPYVSW 14

Db 1 PTHIKW 6

Search completed: November 14, 2004, 13:16:23

Job time: 101 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 14, 2004, 13:03:52; Search time 18:3333 Seconds (without alignments)
78.723 Million cell updates/sec

US-09-831-253F-8 80 Title: Perfect score:

1 EAVLILQGPPYVSWL 15 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

2523 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		. **			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
		38.8	13	7	S47361	T-cell antigen rec
7		33.8	8	~	E47393	neuropeptide calla
٣	25	31.2	15	~	JN0730	hypothetical 1.7K
4		œ	1	0	PH1675	Ig heavy chain V r
2	23	28.7	1	~	JU0356	cycloleonurinin -
9	23	28.7	7	~	PH1676	Ig heavy chain V r
7	23	28.7	13	N	E37390	traA protein - Esc
æ	23	28.7	14	~	PH1677	Ig heavy chain V r
6	23	28.7	14	~	PH1705	Ig heavy chain V r
10	23	28.7	14	7	PT0026	calotropin DI - mu
11	23	28.7	15	~	PA0027	protein_QA100006 -
12	23	28.7	15	~	PH1616	Ig H chain V-D-J r
13	23	28.7	15	7	PH1610	Ig H chain V-D-J r
14	22	27.5	80	7	JS0317	leucokinin VII - M
15	22	27.5	œ	7	A31570	angiotensin-conver
16	22	7	σ	~	S26508	collagen alpha 2(V
17	22	7	10	~	H28027	protein P11 - curl
18	22	7	14	-	LFECW	trp operon leader
19	22	7		~	E90858	trp operon leader
20	22	۲.	14	7	B85761	trp operon leader
21	22	27.5		7	PQ0192	
22	22	7	15	~	PQ0193	stylar glycoprotei
23	22	۲.	15	7	B56046	
24	22	27.5	15	7	PN0662	dystrophin-associa
25	21.5	26.9	15	~	B45115	peptidylprolyl iso
	21	26.2	œ	~	PQ0012	cholecystokinin -
	21	26.2	80	7	A43001	cholecystokinin -
28	21	26.2	80	~	JS0318	leucokinin VIII -
	21	26.2	10	7	A13687	caerulein-like pep

collagen alpha 1(V glutathione transf	lebetin 1 isotorm dystrophin-associa	stylar glycoprotei stylar glycoprotei	dystrophin-associa Ig heavy chain CRD	tryptophyllin, bas T-cell receptor be	phyllocaerulein - Ig H chain V-D-J r	caerulein - frog (	triacylglycerol li Ig heavy chain DJ	bradykinin-potenti
S26506 S17869	S71380 PN0666	PQ0174 PQ0175	PN0665 PT0302	A61081 PT0559	A61357 PH1591	A61337	PC2171 PH1345	хауівн
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26.2	20.00	0,0	9.5	25.0	25.0	0.	25.0	0.
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21	21	21	21 20.5	000	2 20	50	0 0 7 7	20
30	33	35	36	38 39	40	42	4 4 4	45

## ALIGNMENTS

T-cell antigen receptor VJ junction beta chain - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Mo-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999 (Spacession: 847361 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999 (Spacession: 847361 #species to the EMBL Data Library, August 1994 Appearing to the EMBL Data Library, August 1994 Appearing them Human 
Gaps ö 38.8%; Score 31; DB 2; Length 13; 71.4%; Pred. No. 63; 1; Indels 1; Mismatches Query Match
Best Local Similarity 71.4
Matches 5; Conservative

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5 ILOGPPY 11 3 VĽQGSPY 9 ઠે g

neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

CjAccession: E47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. B;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequency A;Reference number: A47393; MUID:93211980; PMID:8460157
A;Accession: E47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>

A;Cross-references: UNIPROT:P41841 A;Experimental source: whole flies A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Gaps ö h Similarity 100.0%; Pred. No. 2.8e+05; 4; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conserva

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1 GPPY 4 a a ઠે

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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: E37390; p00480
C;Accession: E37390; p00480
R;Graus-Geeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
Plasmid 24, 119-131, 1990
A;Title: The sequences of genes bordering oriT in the enterotoxin plasmid P307: comparis
A;Accession: E37390
A;Sterus: preliminary
A;Sterus: preliminary
A;Redecule type: DNA
A;Redidues: 1-13 <GRA>
A;Cross_references: UNIPROT:Q04220; GB:M62986; NID:g150463; PIDN:AAA25525.1; PID:g150468
                                                                                                                                                       Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Preb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
Ciscession: PH1676
R;McHeyzer-Williams M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Bxp. Med. 179, 259-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH1677

Ig heavy chain V region (clone NP-6-6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C;Accession: PH1677

J. Exp. Med. 178, 295-307, 1993

A;Title: Antigen-driven B cell differentiation in vivo.

A;Reference number: PH1675; MUD:93301607; PMID:8315385
                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: PH1676
A;Molecule type: mRNA
A;Residues: 1-13 <MCH>
A;Residues: 10-13 <MCH>
A;Residues: 10-13 <MCH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 13;
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Pred, No. 1.3e+03;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 2; I
Pred. No. 1.3e+03;
3; Mismatches 1;
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C,Superfamily: fimbrial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.7
Best Local Similarity 60.0
Matches 3; Conservative
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A;Residues: 1-14 <MCH>
A;Experimental source: B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:| :||
2 DAILSVQG 9
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QYPPY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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                                                                 Nypothetical 1.7K protein - phage SPP1
NyAlternate names: hypothetical protein 42.1
SigBeclaes: phage SPP1
CipBete: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: JN0730
C;Accession: JN0730
C;Accession: JN0730
C;Accession: JN0730
C;Accession: JN0730
A;Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPP1 (A) A;Accession: JN0730
A;Accession: JN0730
A;Molecule type: DNA
A;Residues: 1-15 cCHA>
A;Cross-references: EMBL:X65941
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C;Species: Leonurus artemisia (sagebrush motherwort)

C;Date: 16-011-1999 #sequence_revision 16-011-1999 #text_change 09-011-2004

C;Accession: 070356

R;Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.

Chem. Pharm. Bull. 39, 712-715, 1991

A;Title: Cycloleonurinin, a cyclic peptide from Leonuri fructus.

A;Reference number: JU0356; MUID:91300597; PMID:2070452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g heavy chain V region (clone NP-6-7) - mouse (fragment)
;Species: Mus musculus (house mouse)
;hate: 24-F91994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
;hacesalon: PH1675
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C,Species: Mus musculus (house mouse)
C,Species: A4-Peb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1
C,Accession: PH1675
R;MCHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1675
A;Accession: PH1675
A;Reference number: B cell
C;Superimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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31.2%; Score 25; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 3; Mismatches 3; Indels
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
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Pred. No. 1.2e+03;
1; Mismatches 1; Indels
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A;Molecule type: protein
A;Residues: 1-12 <KIN>
A;Cross-references: UNIPROT:Q7M1H0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.7%;
80.0%;
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Best Local Similarity 60.0%;
Matches 3; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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1 MLNNGPPFRS 10
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A;Description: Separation and characterization of Arabidopsis proteins by two-dimension A;Reference number: PA0001
A;Reference number: PA0001
A;Accession: PA0027
A;Molecule type: protein
A;Residues: 1-15 < KAM>
A;Experimental source: callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG H chain V-D-J region (clone B-less 30) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHIG16
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Title: Model.18, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tight Chain V-D-J region (wild-type clone 337) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1610
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1610
A;Rocidues: 1-15 <LEV>
A;Residues: 1-15 <LEV>
A;Residues: 1-15 <LEV>
A;Residues: immunoglobulin
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C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0117
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                   28.7%; Score 23; DB 2; 1
45.5%; Pred. No. 1.5e+03;
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                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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75.0%;
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Best Local Similarity 45.5
Matches 5; Conservative
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Matches 3; Conservative
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          submitted to JIPID, July 1994
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1 VLKVYGPXFAS 11
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Matches 4; Conserv
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A,Molecule type: DNA
A,Residues: 1-15 <LEV>
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R;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
B;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
B;Pttochemistry 26, 633-636, 1987
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotro A;Reference number: PT0026
A;Accession: PT0026
A;Accession: PT0026
A;Residues: 1-14 <br/>
BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In the avery chain V region (clone ASC-1) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C; Accession: PH1705
B; McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
B; McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
A; Med: 178, 255-3707, 1939
A; Title: Antigen-driven B cell differentiation in vivo.
A; Reference number: PH1675; MUID:93301607; PMID:8315385
A; Accession: PH1705
A; McHesidues: 114 < MCH>
A; McHesidues: 114 < MCH
A; McHesidues: 114
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0027
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calórcopin DI - mudar (fragment)
C;Species: Calotropis gigantea (mudar, madar)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                           Gaps
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C;Comment: This enzyme is classified as a plant cysteine protease.
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
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0; Mismatches 4; Indels
                                                                                                    Score 23; DB 2; I
Pred. No. 1.4e+03;
1; Mismatches 1;
                                                                                                28.7%;
                                                                                             Query Match
Best.Local Similarity 60.0°
Matches 3; Conservative
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Matches 4; Conservative
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YTSWV 5
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calotropin DI
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Comp. Blochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin A;Reference number: JS0317
A;Accession. JS0317
A;Accession. JS0317
A;Accession. JS0317
A;Residues: 1-8 <HOL>
A;Residues: 1-8 <HOL>
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Kohama, Y.; Mateumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T. Biochem. Blophys. Res. Commun. 155, 332-337, 1988
A.fritele: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle. A.Freference number: A1570; MUID:88326322; PMID:3415688
A.Mocession: A31570
A.Rocession: A31570
A.Cross-references: UNIPROT:P18691
A.Cross-references: UNIPROT:P18691
C.Superfamily: unassigned animal peptides
C; Keywords: angiotensin-converting enzyme inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiotensin-converting enzyme inhibitor - yellowfin tuna
C;Species: Thunnus albacares (yellowfin tuna)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.5%; Score 22; DB 2; Length 8; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 2; Indels
R; Holman, G.M.; Cook, B.J.; Nachman, R.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PPYVSW 14
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2 PAFSSW 7
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0; Gaps

Query Match 27.5%; Score 22; DB 2; Length 8; Best Local Similarity 33.3%; Pred. No. 2.8e+05; Matches 2; Conservative 2; Mismatches 2; Indels

9 PPYVSW 14

| :: | 1 PTHIKW 6

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Search completed: November 14, 2004, 13:17:23 Job time : 19.3333 secs

Appl Appl Appli 
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Sequence
Seq
       Sequence
                                 Sequence
                                                     Sequence
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APPLICANT: Barrett, Ronald W.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gates, Christian
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Hendren, Richard W.
APPLICANT: Hendren, Richard W.
APPLICANT: Hendren, Richard W.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PERTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: PERTIDES AND COMPOUNDS THAT BIND TO A
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 11-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: HTUDIG-C, NUMBER: 96, 392

REFERENCE/DOCKET NUMBER: PK3281

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
US-08-764-640-46
US-08-973-225-46
US-09-224-25-46
US-09-241-704-46
US-09-549-090-46
US-07-807-0318-6
US-08-299-8498-6
US-08-44-318-6
US-08-461-366-6
US-08-461-368-6
US-08-967-727-6
US-08-967-727-6
US-08-037-230D-6
US-08-037-230D-6
US-08-037-230D-6
US-08-037-230D-6
US-09-064-174-2
US-09-064-174-2
US-09-064-174-2
US-09-057-230D-6
US-09-057-230D-6
US-09-057-230D-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 39, Application US/08764640; Patent No. S869451; Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.(
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-764-640-39
    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-764-640-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                      November 14, 2004, 11:57:26; Search time 11.8085 Seconds (without alignments) 84.242 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39,
Sequence 39,
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Sequence 3
Sequence 3
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
                        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-764-640-39
US-08-973-225-39
US-08-973-225-39
US-09-244-298A-39
US-09-549-090-216
US-09-549-090-216
US-09-849-090-216
US-09-849-090-216
US-09-83-230A-39
US-08-956-6631-2
US-08-746-640-37
US-08-746-298A-37
US-09-549-090-37
US-09-832-230A-37
US-09-832-230A-37
US-09-832-230A-37
US-09-832-230A-37
US-09-832-230A-37
US-09-832-230A-37
US-09-832-230A-37
US-08-995-090-10
US-08-985-090-10
US-08-985-090-10
US-08-985-090-10
US-09-165-543-17
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S-08-988-40
S-08-988-090-10
S-08-988-090-16
S-09-165-543-10
S-09-165-543-36
S-09-165-543-36
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3-09-162-368B-19
3-09-161-877B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-271-970-6
US-09-760-397-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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80
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Match Length
                                              Copyright
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Maximum DB seq length: 23
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                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                             Run on:
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No.
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Query Match
Best Local Similarity
Matches 6, Conserva
APPLICANT:
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COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BY PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels
                Length 14;
                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-08-973-225-39
                Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                        Sequence 39, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-973-225-216
Sequence 216, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
                41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 232
            Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                  3 LVGPSLMSWL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NC
COUNTRY: USA
                                                                                                                                                                                        RESULT 2
US-08-973-225-39
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Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                          NUMBER OF SECURIES ADDRESS:
ADDRESSEE Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRYT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTONEY/AGENT INFORMATION:
NAWE: Hubblec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
REGISTRATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 216:
CEPANIENCE PUBLICATION
INFORMATION FOR SEQ ID NO: 216:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.2%; Score 33; DB 3; 60.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Scharz, Peter J.
APPLICANT: Balaeubramanian, Palaniappan
APPLICANT: Hendren, Christopher R.
APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-08-973-225-216
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 39, Application US/09244298A ; Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deprince, Randolph B. Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION UNBER: US 08/973,225
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                        REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 9K326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Dufflin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-549-090-39
; Sequence 39, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-516-704-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 14;
48;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDISC, RODert T.
REGIETRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
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ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                   P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <u >
CLASSIFI
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60.0%; Pred. No. 4
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Hendren, Richard W.
                                                                                                                                                            ZIP: 27709
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-516-704-39; Sequence 39, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                        STREET: Five Moore Drive, P.(CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEOUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-244-298A-39
                                                                                                                                   COUNTRY:
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                                                                                                                                                                           Length 14;
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                                                                                                                                                                         Score 33; DB 3;
Pred. No. 48;
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ATTORNEY/AGENT INFORMATION
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NUMBER OF SEQUENCES: 244
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                         ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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                                   US-09-832-230A-39
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Schatz, Peter J.
Wagetrom, Christopher R.
Wrighton, Nicholas C.
Wrighton: PERTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: PERTIDES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 4; Length 14;
Pred. No. 48;
1; Mismatches 3; Indels
                                                                     Length 14;
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                                                                                                     IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEMTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 13398
                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY APELCATION NUMBER: US 08/973,225
ATTORNEY AGENT INFORMATION:
NAME: HILDIGC, RODERT T.
REGISTRATION NUMBER: 36,392
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1009
                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-549-090-216
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-549-090-39
                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Dufflin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive,
                                                                                                                                                                                                                                     5-09-549-090-216
Sequence 216, Application US/09549090
Patent No. 6465430
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14 amino acids
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                                                                   Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                     6 LQGPPYVSWL 15
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Best Local Similarity
Matches 6; Conserv
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Gaps
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Sequence 39, Application US/09832230A
Patent No. 6506362
GENERAL INFORMATION:
APPLICANT: Dower, William J. et al
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/09428082B

Patent No. 6660843

GENERAL INFORMATION:
APPLICANT: FILU, CHUAN-FA

APPLICANT: LIU, CHUAN-FA

APPLICANT: HIU, CHUAN-FA

APPLICANT: HIU, CHUAN-FA

APPLICANT: HOONE, THOMAS CHARLES

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-5.27

CURRENT APPLICATION NUMBER: US/09/428,082B

CURRENT FILING DATE: 1999-10-22

PRIOR PILLING DATE: 1999-10-23

PRIOR FILLING DATE: 1999-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: P-DOS/MS-DOS
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/832,230A
FILING DATE: 10-Apr-2001
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-832-230A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.2%;
60.0%;
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Barrett, Ronald W
Cwirla, Steven E.
Gates, Christian
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Best Local Similarity 55.6%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 QGPPYVSWL 15
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3 QGPTLTAWL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           COUNTRY: UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-764-640-37
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                                                                                                                                                                                                                                 Sequence 12, Application US/0885663
Patent No. 5849558
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHANGAN, RICHARD
APPLICANT: CHANG, ZHTVUH
TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE
TITLE OF INVENTION: PSPGI RESTRICTION ENDONUCLEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                 Score 33; DB 4; Length 14;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 11; 54;
                                                                                  3; Indels
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                                                                                  1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: New England Biolabs, Inc
STREET: 32 Tozer Road
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE US-09-428-0828-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFFWARE: FASTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,663
FILING DATE: 15-MAY-1997
CLASSIFICATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-764-640-37
; Sequence 37, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 12:
                                               Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Becerly
STATE: MA
COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 978-927-1705
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                    6 LOGPPYVSWL 15
                                                                                                                                                    3 LVGPSLMSWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEQ
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                                                                                                                                                                                                                     US-08-856-663-12
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APPLICANT OWILLS Steven E.

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APPLICANT SHOWS GREEN CONTRICTIONS
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CITY: Research Triangle Park STATE: NC
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 37, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                          NAME: Hrubiec, Robert T.
REGISTRATION UNUBER: 36,392
REFERENCE/DOCKET UNMBER: PK32:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown;
                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
11-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 55.00
-108 Si Conservative
                                                                                                                                                                                                                LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 QGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QGPTLTAWL 11
                                                                                                                                                                                                                                                                                                                           US-09-244-298A-37
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US-09-516-704-37
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Poddturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxn w. . . .
                                                                                                                                    COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEN PC compatible
COMPUTER: BEN PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/06/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, Robert T.
REGISTRATION NUMBER: 36,392
FEFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ 1D NO: 37:
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                                      STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-973-225-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Glaxo Wellcome STREET: Five Moore Drive, P.O. CITY: Research Triangle Park STATE: NC COUNTRY: USA ZIP: 27709 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                STATE: NC COUNTRY: U
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Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
40.0%; Score 32; DB 3; Length 14; 55.6%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: «UNKnown»
ATTORNEY/ACENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
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Search completed: November 14, 2004, 12:08:50 Job time : 12.8085 secs
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park
STATE: NC
COUNTRE READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
TO SO SOFTWARE: DATA: NUMBER: US/09/549,090
FILING APPLICATION DATA:
TO SOFTWARE: PATENTIN TRIBLES TO SOFTWARE: PATENTING TRIBLES TO SOFTWARE TRIBLES TO 
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                                                                                                                                                                                                                                          40.0%; Score 32; DB 3; Length 14; 55.6%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                               3; Indels
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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-549-090-37
;
US-09-516-704-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven B.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/09549090 Patent No. 6465430 GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
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LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schatz, Peter J
                                                                                                                                                                            Query Match
Best Local Similarity 55.0%
Best Local Similarity
Fig. Conservative
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US-09-549-090-37
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3 QGPTLTAWL 11

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November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds (without alignments) 149.815 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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                                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EAVLILOGPPYVSWL 15
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 681, App	Sequence 39, Appl	Sequence 216, App	Sequence 67, Appl	Sequence 67, Appl	Sequence 67, Appl	67,	Sequence 67, Appl	Sequence 67, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 37, Appl	256
SUMMARIES	US-09-833-245-681	US-10-083-768-39	US-10-083-768-216	US-10-609-217-67	US-10-632-388-67	US-10-651-723-67	US-10-645-761-67	US-10-666-696-67	US-10-653-048-67	US-10-006-593-33	US-10-307-724-33	US-10-083-768-37	US-10-424-599-256388
	11	14	14	15	15	12	15	15	15	14	14	14	15
% Query Aatch Length DB	18	14	14	14	14	14	14	14	14	18	18	14	21
% Query Match	42.5	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	40.0	40.0
Score	34	33	33	33	33	33	33	33	33	33	33	32	32
Result No.	-	7	e	4	ហ	9	7	80	σ	10	11	12	13

7 OGPPYVSWL 15 || |: ||| OGCPHPSWL 12

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Sequence 31, Appl	Sequence 10, Appl	Sequence 17, Appl	36,	9 10,	17,	36,	10,	17,	Sequence 36, Appl	e 10	1,	36	'n	0	95	13	25, 1	69	7	Sequence 6, Appli	9	3	46	35		8193	13,	Sequence 9, Appli	Sequence 66, Appl	99	106
US-10-328-916-31	US-09-350-206-10	-03-350-	.09-350-20	-60	.09-349-	US-09-349-755-36	-09-166-		US-09-166-334-36	10-282-9	US-10-282-958-17	US-10-282-958-36	0-422-2	US-10-281-478-23	US-10-281-478-95	-10-	US-10-243-613-25	in	3-0	US-09-760-397-6	10-324-18	-10-006-59	US-10-083-768-46	10-307-7	US-10-378-557-46	US-10-106-698-8193	19-077	US-10-205-150-9	US-10-079-167-66	-10 - 360	US-10-057-475B-10639
15	0	0	σ	σ	σ	σ	σ	σ	σ	14	14	14	14	14	14	14	15	15	10	σ	14	14	14	14	14	14	10	13	14	14	15
22	23	23	23	23	23	23	23	23	23	23	23	23	23	16	16	16	φ	σ	12	15	15	18	18	18	19		σ	6	σ	6	6
40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	39.4	39.4	39.4	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	37.5	37.5	37.5	37.5	37.5
32	32	32	32	32	32	32	32	32	32	32	32	32	32	31.5	31.5	31.5	31	31	31	31	31	31	31	31	31	31	30	30	30	30	30
14	15	16	17	18	19	20	21	22	23	24	25	36	27	. 58	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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LOCATION: (13)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Publication No. US200400101341

Fublication No. US2004001013431

Fublication No. US2004001013431

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REPERENCE: PF546FOT

CURRENT PILING DATE: 2001-04-12

PRIOR PELICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-12-21

PRIOR PILING DATE: 2000-12-21

PRIOR PELICATION NUMBER: 60/199, 384

PRIOR PILING DATE: 2000-04-12

PRIOR PILING DATE: 2000-04-12

PRIOR PELICATION NUMBER: 60/199, 384

PRIOR PILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PALENTING DATE: 2000-04-12

SEQ ID NO 681

LENGTH: 18
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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Publication No. US20040044188A1
GENERAL INFORMATION:
APPLICANT: EDIG. ULRICH
APPLICANT: EDIG. ULRICH
APPLICANT: BOONE, THOMAS CHARLES
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                 NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                      THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 14;
Pred. No. 3.5e+02;
1; Mismatches 3
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Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
ATTORNEY/AGENT INFORMATION:
NAME: HITDLEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/609,217
CURRENT FILING DATE: 2003-06-27
PRIOR PAPLICATION NUMBER: US/09/428,082B
PRIOR PILING DATE: 1999-10-22
PRIOR PILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: Patentin version 3.1
SEQ ID NO ED IN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
; CTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-609-217-67
                                                                                                                                                             COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.0
Matches 6; Conservative
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LVGPSLMSWL 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.2%; Score 33; DB 14; Length 14; 60.0%; Pred. No. 3.5e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER RADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-083-768-39
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSER: Glaxo Wellcome
STREET: Five Moore Drive, P.O.
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christopher R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 216, Application US/10083768
Publication No. US20030158116A1
GENERAL INFORMATION:
APPLICANT: Dower, William J.
CWAITA, Seven E.
Duffin, David J.
                                     Sequence 39, Application US/10083768
Publication No. US20030158116A1
GENERAL INFORMATION:
BATTEL, William J.
BATTEL, Steven B.
CWITIA, Steven B.
Duffin, David J.
                                                                                                                                                                                                                                       Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                 Haselden, Sherril S.
                                                                                                                                                                                             Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Best Local Similarity
Matches 6; Conservi
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US-10-083-768-216
RESULT 2
US-10-083-768-39
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Gape ; 0

Length 14; 3; Indels

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Gaps
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                                                                                                                                                                     Sequence 67, Application US/10645761
| Sequence 67, Application US/10645761
| Publication No. US20040071712A1
| GENERAL INFORMATION:
| APPLICANT: FIGURATION:
| APPLICANT: BIGE, ULRICH
| APPLICANT: BOONE, THOMAS CHRELS
| APPLICANT: BOONE, THOMAS CHRELS
| TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
| TITLE OF INVENTION WOBER: US/10/645,761
| CURRENT FILING DATE: 2003-08-18
| PRIOR PAPLICATION NUMBER: US/09/428,082B
| PRIOR PLING DATE: 1999-10-22
| PRIOR APPLICATION NUMBER: 60/105,371
| PRIOR APPLICATION NUMBER: 60/105,371
| PRIOR PLING DATE: 1998-10-23
| NUMBER OF SEQ ID NOS: 1133
| SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FIGURE ULRICH
APPLICANT: ENGS. ULRICH
APPLICANT: ELU, CHUAN-FA
APPLICANT: HIU, CHUAN-FA
APPLICANT: HIU, CHUAN-FA
APPLICANT: GHESTHAM, JANET C.
APPLICANT: GUDAS, JEAN MARIB
ITLEO POR INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-5.79
CURRENT PILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/563,286C
PRIOR FILING DATE: 2000-05-03
PRIOR PILING DATE: 1999-10-23
PRIOR PILING DATE: 1999-10-23
PRIOR PILING DATE: 1999-10-23
PRIOR PILING DATE: 1998-10-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 15; Length 14;
Pred. No. 3.5e+02;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: TPO-MIMETIC PEPTIDE US-10-645-761-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: TPO-mimetic peptide US-10-666-696-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-666-696-67
; Sequence 67, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0.
                       6 LOGPPYVSWL 15
                                                               3 LVGPSLMSWL 12
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                                                                                                                                  RESULT 7
US-10-645-761-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 67
LENGTH: 14
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LENGTH: 14
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                                                                                                                                                                                                                                                            APPLICANT: FEIGE, ULRICH
APPLICANT: FEIGE, ULRICH
APPLICANT: CHENAL-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: CHEETHAM, JANET C.
APPLICANT: HOWAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT APPLICATION NUMBER: US/09/428,082B
PRIOR PILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1999-110-33
NUMBER OF SEQ ID NOS: 11133
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, LATU, CHUAN-FA
APPLICANT: CHEETHAM, LATURAN CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/651,723
CURRENT FILING DATE: 2003-08-29
FRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
FRIOR FILING DATE: 1999-10-23
FRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTIN VEXESON 3.1
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  3; Indels
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Pred. No. 3.5e+02;
1; Mismatches 3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: TPO-MIMETIC PEPTIDE US-10-632-388-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: TPO-MIMETIC PEPTIDE US-10-651-723-67
                                                                                                                                                                                          Sequence 67, Application US/10632388
Publication No. US20040053845A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/10651723
Publication No. US20040057953A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
6; Conservative
                                                                        3 LVGPSLMSWL 12
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                                            LOGPPYVSWL 15
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                            US-10-632-388-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 67
LENGTH: 14
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Matches
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Wrighton, Nicholas C.
TILLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.2%; Score 33; DB 14; Length 18; 41.7%; Pred. No. 4.4e+02;
                        Indels
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                                                                                                                                                                                                                                                                                                          APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR PILING DATE: 2001-12-05
PRIOR PLING DATE: 2001-05-04
PRIOR PLING DATE: 2001-05-29
PRIOR PRILING DATE: 2001-05-29
PRIOR PRILING DATE: 2001-05-29
PRIOR PLING DATE: 2001-05-29
PRIOR PLING DATE: 2001-05-29
PRIOR PLING DATE: 2001-05-39
PRIOR PLING DATE: 2001-12-05
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    Pred. No. 4.4e+02;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENČE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                            ; Sequence 33, Application US/10307724; Publication No. US20030232972A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schatz, Peter J
  Best Local Similarity 41.7%;
Matches 5, Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 232
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ZIP: 27709
COMPUTER READABLE FORM:
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Best Local Similarity 41.7
Matches 5, Conservative
                                                                          4 LILOGPPYVSWL 15
                                                                                                                       1 MIIEGPILROWL 12
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1 MIIEGPTLRQWL 12
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; bublication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FIGE, ULRICH
; APPLICANT: ELU, CHUAN-FA
; APPLICANT: CHETHAM, JANET C.
; APPLICANT: BOONE, THOWAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1999-10-23
; NUMBER OF SEQ ID NOS: 1133
; NUMBER OF SEQ ID NOS: 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.2%; Score 33; DB 15; Length 14; 60.0%; Pred. No. 3.5e+02; tive 1; Mismatches 3; Indels
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                           Indels
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Sequence 33, Application US/10006593

Publication No. US20030049683A1

GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.

APPLICANT: Renshaw, Mark

TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES

FILE REFERENCE: 1087-2

CURRENT APPLICATION NUMBER: US/10/006,593

CURRENT FILING DATE: 2001-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2001-05-04

PRIOR PILING DATE: 2010-05-04

PRIOR PILING DATE: 2010-05-04

NUMBER: OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.1

SEQ ID NO 3: LENTING DATE: 2011-05-04

SEQ ID NOS: 118

LENTING NOS: 118
  60.0%; Pred. No. 3.5e+02;
tive 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 60.0.
Best Local Similarity 60.0
Matches 6; Conservative
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                                                                        6 LOGPPYVSWL 15
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LENGTH: 14
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TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor TITLE OF INVENTION: Involved in Islet Cell Signaling FILE REPERBERGE: 016325-0072100S
CURRENT APPLICATION NUMBER: US/10/328,916
PRIOR APPLICATION NUMBER: US 60/345,697
PRIOR APPLICATION NUMBER: US 60/345,697
PRIOR FILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN Ver. 2.1
ENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:mouse IC-GPCR; OTHER INFORMATION: Transmembrane IV domain
US-10-328-916-31
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Patent No. US20020099199A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTOR: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 15; Length 22;
Pred. No. 7.6e+02;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEFRAE: (617)227-7400
TELEFRAE: (617)227-7400
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
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50.0%;
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ORGANISM: Artificial Sequence
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MEDIUM TYPE: Floppy disk
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LENGTH: 23 amino acids
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Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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COUNTRY: USA
ZIP: 02109
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FRAGMENT TYPE:
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 256388
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40.0%; Score 32; DB 14; Length 14;
Best Local Similarity 55.6%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels
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    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_73542C.1.pep
US-10-424-599-256388
                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTATION UNUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-083-768-37
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Publication No. US20040002114A1
GENERAL INFORMATION:
APPLICANT: Gregoire, Francine M.
APPLICANT: Ofonson, Jeffrey D.
APPLICANT: Blume, John E.
APPLICANT: Metabolex, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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Best Local Similarity 50.0
Matches 5; Conservative
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5 ILQGPPYVSW 14 :| || :|| 14 LLYGPAILSW 23

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Search completed: November 14, 2004, 12:27:00 Job time : 36.4255 secs

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November 14, 2004, 11:57:25; Search time 43.4043 Seconds (without alignments) 123.973 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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80
                Copyright
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seq length: 23
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Maximum I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\*

geneseqp2004s:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_23Sep04: geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\*

Database :

Description	Aay92952 Transform Aay93104 Transform		4.00	Aaw16483 INLOMDODO Aaw36634 Thrombopo Aaw36767 Thrombopo		Abb72897 TPO mimet Adj73048 TPO mimet	CH1 Huma	10 m s	Adroszeu N-termina Adko3181 Hepatitis Adko3184 Hepatitis	
SUMMARIES	AAY92952 AAY93104	AMI33812 ADF14790 AME01738	ABG63934 ADL77199	AAW36634 AAW36634 AAW36767	AAU25853	ABB72897 ADJ73048	ADJ51644 ABB05646	ABP51685 ADQ16613	AAKSSZ6U ADK03181 ADK03184	AAW83368 AAW09481 AAW36632
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Length	15	13	18 18	7 7 7	14	444	14 15	18	y 6	1111
* Query Match	100.0	43.1	42.5	4 4 4	41.2	41.2	41.2	41.2	4 4 4 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	40.0 40.0
Score	80		ው E. C	1 E E	) E E		. e. e.	333	9 8 8	32 33 35
Result No.	100	ህ <b>4</b> ሺ	φ r c	9 6	112	113	16	138	21 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	23 24 25

		Agg67849 Partial r Abg76410 Human mus Abg76414 Rat musca Abg76417 Rat musca Adj55648 Short enz	Addingson Amingin Pep Addingson Murine AX Addingson Murine AX Addingson Murine AX Abrison AMP-2 sel Adk14204 Matrix me
4 AAU25851 5 AAU97014 8 ADM12614 8 AD038847	5 ABP48149 2 AAW92981 2 AAW92987 2 AAG67842 2 AAG67835	2 AAG67849 6 ABG76410 6 ABG76424 6 ABG76417 8 ADJ55648	4 ADC99952 7 ADC99989 7 ADC9988 7 ADC99880 6 ABR55023 8 ADK14204
	40.0 18 40.0 23 40.0 23 40.0 23	40.0 23 40.0 23 40.0 23 40.0 23	399.44 116 399.44 116 399.64 116 399.66 6
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26 27 28 29			7 4 4 4 4 4 7 4 6 4 4 4 5

## ALIGNMENTS

Hepatotropic, antagonist, transforming growth factor betal, TGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis. Transforming growth factor inhibitory peptide #8. Ş AAY92952 standard; peptide; 15 99WO-ES000375. 98ES-00002465. (first entry) WO200031135-A1. Homo sapiens. 23-NOV-1999; 24-NOV-1998; 08-NOV-2000 02-JUN-2000. AAY92952; AAY92952 

(CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Claim 9; Page 82; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of srimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DMA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

us-09-831-253f-8.rag

RESULT 2 AAY93104

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signal peptide that is the same as the native signal peptide except that the 3 C-terminal amino acid residues are Ser-Trp-Ser The invention is directed to glycosylated leptin proteins (see AAA95799-804) that have a Stokes' radius greater than that of naturally occurring human leptin. A claimed method for manufacturing a glycosylated leptin involves culturing a host cell containing a DNA sequence encoding a signal peptide and a glycosylated leptin protein. Preferred signal peptides have a peptidase cleavage site optimized for glycosylation efficiency. When leptin+459+102 (see AAY95802) was expressed as a fusion with the present signal peptide, the degree of glycosylation (on a scale of 1-5) was 3.5 in COS host cells and 4 in CHO host cells. Glycosylated leptins, or nucleic acids encoding them, are used in the treatment of obesity, diabetes and the effects of high blood lipid content (claimed). They have longer systemic circulation times in vivo than native leptins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosylated leptin proteins having a Stokes' radius greater than that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is that of a human tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a naturally occurring glycosylated human leptin useful for treating obesity, diabetes and the effects of high blood lipid content.
                                                                                                                                                                                                        antiobesity, antidiabetic, hyperlipemic; therapy, signal peptide;
tissue plasminogen activator; mutant; mutein.
                                                                                                                                                                                     Leptin; human; glycosylation; obesity; diabetes; hyperlipidemia;
                                                                                                                                             Modified human tissue plasminogen activator signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 14; Page 99; 156pp; English.
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                     AAY95812 standard; peptide; 23 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-2000; 2000WO-US003652.
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                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elliott SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-524540/47.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 AA;
                                                                                                                                                                                                                                                                                                                                 WO200047741-A1
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                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                     07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martin FH,
                                                                                                                                                                                                                                                                                             Synthetic.
                                                           AAY95812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatotropic, antagonist, transforming growth factor betal, TGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lasarte Sagastibelza JJ, Prieto Valtuena J;
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                                                               Length 15;
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                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor inhibitory peptide P150.
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                                                           Score 80; DB 3; I
Pred. No. 7.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 80; DB 3; 1
Pred. No. 7.9e-06;
; Mismatches 0;
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                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 33; 86pp; Spanish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression systems) encoding the
disease, specifically cirrhosis
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                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                    Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                             1 EAVLILOGPPYVSWL
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
                     Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-1999;
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                                    Gaps
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   Length 23;
Score 36; DB 3; Length 23;
Pred. No. 1.3e+02;
Mismatches 3; Indels
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RESULT 3

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chemotaxis; food additive; binding partner identification.
                                                  Homo sapiens
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ABG63934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel peptide or epitope which is prone to deamidation by tissue transglutaminase (tTG) and is a causative factor of cellac disease (CD, gluten intolerance) or an autoimmune disease such as rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, sjogren syndrome or diabetes. The peptide of the invention demonstrates immunosuppressive, antirheumatic, antiarchritic, antidiabetic, dermatological and antiinflammatory activities whilst pharmaceutical compositions comprising the peptides or epitopes may be useful for the treatment of a celiac disease or an autoimmune disease such as rheumatoid
plant; deamidation; tissue transglutaminase; tTG; celiac disease; CD; gluten introlerance; autoimmune; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; sjogren syndrome; diabetes; immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      current sequence is that of the diabetes autoantigen-derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; proliferative disorder; cancer; tumour; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriaeis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis, multiple sclerosis, systemic lupus erythematosus, sjogren syndrome or diabetes. Glucen-derived peptides may be useful in the preparation of therapeutic agents capable of eliminating subset of cells, particularly gluten-sensitive or auto-antigen sensitive r cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 19 encoded secreted protein HYASC80 fragment, SEQ ID NO:151
                                                                                                                                                                                                                                                                                                                                                                                                                        New gluten peptides or epitopes prone to deamidation by tissue
transglutaminase, useful for treating celiac disease or an autoimmune
disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 285; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE01738 standard; peptide; 18 AA.
                                                                                     dermatological; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                          (ZIEK-) ACAD ZIEKENHUIS LEIDEN
                                                                                                                                                                                                                                                                                                04-FEB-2002; 2002EP-00075456.
                                                                                                                                                                                                                                                       04-FEB-2002; 2002EP-00075456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erythematosus, or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AVLI-LQGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-647889/62.
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                                                                                                                                                                   EP1332760-A1
                                                                                                                            Unidentified
                                                                                                                                                                                                             06-AUG-2003
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AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted

protein genes, and AAE01672-AAE01743 represent the proteins they encode.

AAE01744-AAE01751 represent human secreted protein fragments or variants.

CT he secreted proteins and their genes are useful for preventing, treating
or ameliorating medical conditions, e.g., by protein or gene therapy.

Extendedical conditions can be diagnosed by determining the amount of the
new protein in a sample or by determining the presence of mutations in
the new genes. Specific uses are described for each of the 22 genes,
consection that issues in which they are most highly expressed, and include
developing products for the diagnosis or treatment of proliferative
developing products for the diagnosis or treatment of proliferative
cdeveloping products for the diagnosis or treatment of proliferative
disorders, cancer, tumours, foetal and developmental abnormalities,
cancer, the control of arthritis), inflammation, allergies,
control of the control of arthritis), inflammation, allergies,
control disorders, diabetes, atherosclerosis, cardiovascular disorders,
control of sepsis, diabetes, atherosclerosis, cardiovascular disorders,
pregnancy-related disorders, atherosclerosis, action disorders,
contributed isorders, kidney disorders, gastrointestinal disorders,
pregnancy-related disorders, and con the allowand soft primary tissues,
contributed in sorders, to identify their cognate ligands or binding
contributed to modify storage properties. Antibodies specific for a
contributed invention can be used as a food additive or
contributed invention can be used as a food additive or
contributed envention can be used as a food additive or
contributed envention can be used as a food additive or
contributed envention can be used an in diagnostic immunosassy or enzyme linked immunosorbent assay (ELISA). The
contributed invention as home and in diagnostic immunosassy or enzyme linked immunosorbent assay (ELISA). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 2.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olsen HS, Ruben SM;
                                                                          /label= Unknown
/note= "Encoded by MTM"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 514; 540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1999; 99US-0163576P.
27-JUL-2000; 2000US-0221366P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                         11-NOV-2000; 2000WO-US030036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soppet DR, Komatsoulis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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Best Local Similarity
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                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                            WO200134767-A2
                                                                                                                                                                                                                                                                                               17-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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ò а Albumin fusion protein related therapeutic protein X, SEQ ID No 681 albumin fusion protein; cytostatic; antianaemic; antiarthritic;

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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HBA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders ench as cancer, reproductive disorders, disestes (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheinmer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).

ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.
                                                                                                                                         Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haemacropoletic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunemodulator; anti-HIV; antiinflammatory; antiulcer; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 5; Le:
Pred. No. 2.1e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 912; 2102pp; English
                                                                                                         Human albumin fusion protein #609.
ABG63934 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2001; 2001WO-US011988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMA-) HUMAN GENOME SCI INC
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-010886/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                      WO200177137-A1.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2000;
                                                                    27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001
                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
                                  ABG63934;
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The invention relates to a novel albumin fusion protein. The invention further relates to: a composition comprising the albumin fusion protein and a pharmaceutical carities; a kit comprising the albumin fusion protein cormula; a method of treating a disease or albumin fusion protein; a method of treating a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polymucleotide fragment or variant; a nucleic acid molecule comprising a polymucleotide comprising the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following activities: expositefuc, antianaemic, antiarthing and a host cell activities: expositefuc, antianaemic, antiarthing antiarchmatic, antiarchmatic, costeopathic, dermatological, antiinflammatory, antipsoriatic, antidiabetic, antidiabetic
                                                                                     antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory; antisethmatic; anti-HIV; immunosuppressive; antiinflammatory; antipproriatic; antibacterial; osteopathic; dermatological; antigout; immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer; antidabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer; reproductive system disorder; therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome, Down's syndrome, Parau syndrome, Turner's syndrome, Apert syndrome or Tay Sachs disease), excretory diseases (e.g. urinary incontinence, urinary tract infections or renal diseorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New albumin fusion proteins, useful for diagnosing, treating,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 681; 279pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001; 2001US-00833245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROSEN C A.
HASELTINE W A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-090519/09.
                                                                                                                                                                                                                                                                                                                                US2004010134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSE/) ROSEN C
(HASE/) HASELTIN
                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004.
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Gaps

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Indels

6; Conservative

Best Loca Matches

15

7 QGPPYVSWL

OGCPHPSWL 12

g 8

ADL77199 standard; peptide; 18 AA.

RESULT 7 ADL77199 20-MAY-2004 (first entry)

ADL77199;

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41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                              6 LQGPPYVSWL 15
                                                            | || :|||
LVGPSLMSWL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVGPSLMSWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052226/05.
            Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Barret
LC, Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14 AA;
                                                                                                                                                                                                                                                                                               WO9640750-A1
                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                     11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mattheakis
                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                AAW36634;
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   Query Match
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                                                                                                              AAW36634
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         compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This sequence represents a therapeutic protein X relating to the albumin fusion protein of the invention. The sequence listing data for this specification was dowloaded from the USPTO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a peptide which binds to thrombopoietin (TDO) receptor (TR). The compound can be used for treating patients suffering from hammatological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bome marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson SS;
                                                                                                                                                                     Gaps
  cerebellar ataxia, attention deficit disorder, autism or obsessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                 Score 34; DB 8; Length 15;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                               Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duffin DJ, Gates'n CR, Wrighton NC;
                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barrett RW, Cwirla SE, Duffi
LC, Schatz PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                         Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 26; 106pp; English.
                                                                                                                                                                                                                                                                      AAW09483 standard; protein; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO receptors on living cells
                                                                                                                                              42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US008998
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                            15
                                                                                                                                                                                                                 OGCPHPSWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-051883/05.
                                                                                                                                                                                          7 OGPPYVSWL
                                                                                                                                                       Best Local Similarity
                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattheakis LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CM, Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 17, Pred. No. 2.4e+02; 3; Indels
Score 33; DB 2; Length 14;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             et RW, Cwirla SE, Duffin DJ, Gates Cl
Schatz PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 26; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                AAW36634 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US009623.
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Local Similarity
                                                                                                                                                             (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 AA;
                                                               WO200024782-A2
                                                                                                                                                                                   Feige U, Liu
                                                                                                         25-OCT-1999;
                                                                                                                             23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-2001
                                                                                                                                         22-OCT-1999;
                                                                                    04-MAY-2000
                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used disgnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autodimune disease; cytostatic; antiackhmatic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antiagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                                                                                                                                                                                                                                                                                       Johnson SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                    thrombopoietin receptor – useful in treatment of haematological
disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                  Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                          Peptides and peptide mimetics which bind to and activate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 2; Length 14;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                     Cwirla SE, Duffin DJ, Gates CM, PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:67.
                              Thrombopoietin receptor binding peptide.
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 75; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17011 standard; peptide; 14 AA
                                                                                                                                                              /note= "NH2-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.2%;
                                                                                                                                                                                                                                                95US-00478128
95US-00485301
                                                                                                                                                                                                                           96WO-US009623
           (first entry)
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                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                     Dower WJ, Barret RW,
Mattheakis LC, Schatz
                                                                                                                                         1. .14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVGPSLMSWL
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14 AA;
                                                                                                                                      Disulfide-bond
Modified-site
                                                                                                                                                                                  WO9640750-A1
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           11-MAR-1998
                                                                                                                                                                                                        19-DEC-1996
                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB17011;
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The present invention describes composition of matter (I) comprising an CF domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an C domain; X1 and X2 = are each
independently selected from -(II)C-P1, -(II)C-P1-(L2)d-P2, -(IL)C-P1-
(IL2)d-P2-(L3)e-P<sup>3</sup>; or -(IL)-P1-(L2)d-P3-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active C peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, C c, d, e, and f = are each independently or 1, provided that at least 1 c peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, C c and b is 1. The composition can have cytostatic, antisathmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions cuch as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent uncleotide and amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; boom marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 3; I
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Page 217; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0105371P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00428082
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antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO mimetic peptide sequence SegID 502
                                                                                                                                                                                                                                                                                                           WPI; 2002-130313/17.
                                                                        Fanconi's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                Peige U, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 AA;
                                                                                                                                        WO200183525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                  Homo sapiens
                                                                                                                                                                    08-NOV-2001.
                                                                                                                Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BXBXXX
                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells compracted contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situate taining, fluorescence-activated cell sorting, Western blotting and centre candom materials. They may also be used for in situate dimmunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TTNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
                                                                                                                                                                                                           Schatz PJ;
Deprince RB, Podduturi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
                                                                                                                                                                                                                                                                                                           cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                          Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cowith peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 4; Length 14;
Pred. No. 2.4e+02;
.; Mismatches 3; Indels
                                                                                                                                                                                                         Barrett RW, Cwirla SE, Gates CM, unian P, Wagstrom CR, Hendren RW,
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 20; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB72897 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO mimetic peptide SEQ ID NO:67.
                                                                                01-MAR-2000; 2000US-00516704.
                                                                                                                       95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.2%;
                                                                                                             95US-00478128.
                                                                                                                                                    96US-00699027
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                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                         Dower WJ, Barrett F
Balasubramanian P,
                                                                                                                                                                                                                                                                WPI; 2001-564142/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 AA;
 Homo sapiens.
                           US6251864-B1
                                                                                                          07-JUN-1995;
                                                                                                                                       07-JUN-1996;
                                                                                                                                                    15-AUG-1996;
                                                     26-JUN-2001
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                                                                                                                                                                                                                                      Yin Q;
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ultimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic antiarthritic, antidiabetic, ophthalmological, antitheumatic, antiarthritic, antidiabetic, ophthalmological, cantendectic, antirheumatic, antidiabetic, dermatological antiansemic, anorectic, antinherthilty, haemostatic, dermatological antiansemic, anorectic, antinherthilty, haemostatic of antiophylactic agent as well as for screening purposes. (I) is useful for diagnostic agents of an ideases characterised by dysfunction of their sesociated protein of interest, for identifying normal or abnormal proteins of interest in a blological sample. Additionally, (I) is useful for treating interest in a blological sample, Additionally, (I) is useful for treating inflammatory and autonimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, inflammatory and autonimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, inflammatory and servological degenerative diseases. (I), comprising for mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or and servinement antion of the present invention expensed in the present invention
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neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; htbumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes a vehicle-peptide molecule (I) or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gudas JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Page 44; 176pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2001; 2001WO-US014310.
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This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of fragment where a protein, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibodies, so including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody of suggeth symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobal, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a minetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                 mimetic, CDR mimetibody, gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 7; Length 14;
Pred. No. 2.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                     Ghrayeb J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH1 deleted mimetibody-related peptide SegID502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 502; 97pp; English.
                                                                                                                                                                                                                                                                                                                                       Scallon BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ52683 standard; peptide; 14 AA.
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                                                                                                                                                                                                                         24-MAR-2003; 2003WO-US009139
                                                                                                                                                                                                                                                            29-MAR-2002; 2002US-0368791P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                       Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LQGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LVGPSLMSWL 12
                                                                                                                                                                                                                                                                                                (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-804237/75.
                                                                                                                                                WO2003084477-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                    16-OCT-2003
                                                                                                                                                                                                                                                                                                                                       Heavner GA,
                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ52683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiant, hypotensive, neuroprotective, nootropic, cardiavascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, is useful for diagnosing or treating a disease condition in a cell, is useful for diagnosing or treating a disease condition on a cell, is useful for diagnosing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases (for example bacterial, viral or conditions, or infectioned diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                        New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                  Ghrayeb J, Scallon BJ, Nesspor TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 502; 129pp; English.
viral infection; fungal infection.
                                                                                                                                                                                                   27-JUN-2003; 2003WO-US020347.
                                                                                                                                                                                                                                            28-JUN-2002; 2002US-0392431P.
                                                                                                                                                                                                                                                                                                                                Knight DM,
                                                                                                                                                                                                                                                                                       (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-082870/08.
                                                                                                            WO2004002417-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                         Kutoloski KA;
                                             Unidentified
                                                                                                                                                          08-JAN-2004.
                                                                                                                                                                                                                                                                                                                             Heavner GA,
                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases.
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Gaps

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Length 14; 3; Indels

Score 33; DB 8; I Pred. No. 2.4e+02; Mismatches

41.2%;

6; Conservative

Local Similarity

Query Match Matches

ઠે 엄 Search completed: November 14, 2004, 12:02:16

Job time : 45.4043 secs

CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Altheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;

Q7m1h0 leonurus ar Q0420 plaemaid p30 P20728 calotropis P81801 streptomyce Q9820 hordeum vul G01db6 mus sp. mac Aag38018 mus muscu Aap13932 mus sp. m Q75.67 conger myri Q75.f1 conger myri Q75.f2 conger myri

Run on:

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Porphyra purpurea.
Mitochondrion.
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
MCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbosa A., Demeure O., Urien C., Milan D., Chardon P., Renard Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ629179; CAF32800.1; -.
NON_TER 1 1 1 1
NON_TER 23 23
SEQUENCE 23 AA; 2574 MW; 0B078824AA2E0517 CRC64;
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Pred. No. 3.9e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Lang B.Franz., Goff L.J., Gray M.W.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U59763, AABL7951.1; -
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA; 1522 MW; 0831666D0E8C65B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Q8XXZ2
Q7M1H0
Q04120
Q04120
CALI CALGI
P818G1
Q9S8Z0
Q6LDB6
AAG139018
AAF13932
Q75K67
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytochrome oxidase subunit 3 (Fragment)
Name=cox3;
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                                                                                                                                                            Q75RF1
Q75RM2
Q75RS8
Q75RT8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0700R6;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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 228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.228.77.22
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SEQUENCE
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P41841 calliphora
P83647 oryza sativ
O9rrg1 oncorhynchu
O9rrg1 oncorhynchu
O9rrg1 oncorhynchu
O9rg26 box taurus
O9f71 honco sapien
O26075 psammechinu
O6nt60 homo sapien
Anh69320 homo sapien
Ash69320 homo sapien
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sepia offic
candida alb
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                5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                             1825181 segs, 575374646 residues
               GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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PIL3_ECOLI
Q7SO06
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Maximum Match 100%
Listing first 45 summaries
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Q9UR76
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Q26075
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AAH69320
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Gapop 10.0 , Gapext 0.5
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Q7M1G0
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Q8NED5
Q85481
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Perfect score:
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Result

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Local Similarity 43.8 ses 7; Conservative
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NCBI_TaxID=2782,
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                       Gaps
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Barbosa A., Demeure O., Urien C., Milan D., Chardon P., Renard C.;

"A physical map of large segments of pig chromosome 7q1.1-q1.4:
comparative analysis with human chromosome 6p21.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ629179; CAF32800.1; -.
                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 2; Length 23; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.2%; Score 29; DB 2; Length 13; 42.9%; Pred. No. 8.5e+02; tive 3; Mismatches 1; Indels
  Length 23;
                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lang B.Franz., Goff L.J., Gray M.W.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U59764, ABB17950.1, -.
GO, GO:0005739, C:mitochondrion, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .tochondrion.
NN_TER 1 1 305BD4028745B043 CRC64;
                                                                                                                                                                                                                                                                                                                               23 AA; 2574 MW; 0B078824AA2E0517 CRC64;
                                                                                                                                     03-MAR-2004 (TrEMBLrel. 27, Created)
03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome oxidase subunit 3 (Fragment).
 Score 31; DB 2;
Pred. No. 7e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AA.
                                                                                                                  23 AA.
                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                      Fas binding protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                   38.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gracilariopsis lemaneiformis
Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.9%;
Matches 3; Conservative
                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             6 LOGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                         11 LQNPPKPPWI 20
                                          6 LQGPPYVSWL 15
                                                              11 LONPPKPPWI
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Best Local Similarity
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PNYITWI 7
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SEQUENCE
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SEQUENCE
                                                                                                                  CAF32800
CAF32800;
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CAF32800
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                                                                                                                                                           Rattus sp. .
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae; Murinae, Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                          MEDLINE=96278823; PubMed=8662884;
Chernousov M.A., Stahl R.C., Carey D.J.;
"Schwann cells secrete a novel collagen-like adhesive protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Last Sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Melittin-like peptide (MLP).
Bana temporaria (European common frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Blochem. 242:788-792(1996).
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUB SPECIFICITY: Skin.
Amidation; Amphibian defense peptide; Direct protein sequencing.
MOD RES 22
SEQÜENCE 22 AA; 2313 MW; 0990320F9B0709B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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7
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MEDLINE=97175050; PubMed=9022710;
Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 29; DB 2; Length 16; 100.0%; Pred. No. 1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 29; DB 1; Length 22; 43.8%; Pred. No. 1.5e+03;
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                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2000 (TrEMBLrel. 14, Last annotation update)
Collagen-like heparin-binding glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 271:13844-13853(1996).
SEQUENCE 16 AA; 1329 MW; 0F03A38D20A9221C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA.
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16 AA
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SOVO SEPOF
1D SOVO SEPOF
80VO SEPOF
80VO SEPOF
1D 29-MAR-2004 (Rel. 43, Created)
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Local Similarity 50.0
nes 6; Conservative
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LLINOPKY-SWL 13
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                        NCBI_TaxID=72011;
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                                                                                                                                                                                                                                                                             Query Match
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CALVO
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Aldehyde dehydrogenase family 7 member Al (EC 1.2.1.3) (Antiquitin 1)
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE=94156217; PubMed=8075797;
MeDLINE=94156217; PubMed=8075797;
Molloy C., Cannon R.D., Sullivan P.A., Shepherd M.G.;
"Purification and characterization of two forms of N-
acetylglucosaminidase from Candida albicans showing widely different
outer chain glycosylation.";
Microbiology 140:1543-1533(1994).
SEQUENCE 20 AA; 2178 MW; DA602087EDDB4047 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                    Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                        FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
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Pred. No. 1.2e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 2; Length 20;
Pred. No. 1.9e+03;
1; Mismatches 5; Indels
                                                                                                                                                                                                          13 13 Tyrosine amide.
13 AA; 1503 MW; 483D5C7B34C72727 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
29-MAR-2004 (Rel. 43, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              20 AA.
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                                                                                                                                                                                               Amidation, Direct protein sequencing.
                          Sepia officinalis (Common cuttlefish)
                                                                                                                                                                                                                                                                                                                                                                                           N-acetylglucosaminidase A (Fragment)
Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                Created)
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50.0%;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                         5; Conservative
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                                                                                            TISSUE=Ovarian follicle;
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                            1 EAVLILOGPPY 11
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Matches 5; Conserv
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                  SepOvotropin.
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ID D7A1_ACASC
AC P83402;
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SEQUENCE
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Matches
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TISSUB-Liver;

MEDLINE=21956475; PubMed=11959129;

Tang W.-K., Chang C.H.K., Fong W.-P.;

"First purification of the antiquitin protein and demonstration of its
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazaa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzymatic activity.";
FBBS Lett. 516:183-186(2002).
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;

[Hyp3]Met-callatostatin. Identification and biological properties of a novel neuropeptide from the blowfly Calliphora vomitoria.";

J. Biol. Chem. 269:21059-21066 (1994).

-!- FUNCTION: May act as a neurotransmitter or neuromodulator and play a role in the integration of information within the brain. May be involved in the control of visceral muscles due to its ability to behave as potent inhibitors of peristalic movements. May also thifill a neurohormonal role on muscles of the gut and heart.
-!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
                             Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Percoidei,
Sparidae, Acanthopagrus.
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"Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence homology to cockroach allatostatins.";
Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - SUBUNIT: Honotetramer.
- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde mm and Vmax is 1.3 micromol/min x mg enzyme.
- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
GO; GO:0004029; F:aldehyde dehydrogenase (NAD) activity; IDA.
GO; GO:0006081; P:aldehyde metabolism; IDA.
InterPro; IPR002086; Aldehyde metabolism; IDA.
PROSITE; PS000070; ALDEHYDE_DEHYDR_CGLU; PARTIAL.
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NON TER 18
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                                                                                                                                                                                                                                                                               SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT
Acanthopagrus schlegeli (Black porgy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION, AND HYDROXYLATION.
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RESULT 11

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mypothetical protein (Fragment).
Micotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Etreptophyta; Embryophyta; Tracheophyta; Spermatcophyta; Magnoliophyta; eudicotyledons; core eudicote; asteride; lamiide; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-20023723; PubMed=10561067;
Foster E., Hattori J., Labbe H., Ouellet T., Fobert P.R., James L.E.,
Iyer V.N., Miki B.L.,
"A tobacco cryptic constitutive promoter, tCUP, revealed by T-DNA
                                                                                            Yamashita M., Ojima N., Sakamoto T.; "Induction of proteins in response to cold acclimation of rainbow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96126798; PubMed=8564801;
Punzi J.S., DenBesten P.K.;
"Purification of nonamelogenin proteins from bovine secretory
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                        Score 27; DB 2; Length 21; Pred. No. 3e+03; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enamel.";
Calcif. Tissue Int. 57:379-384(1995).
SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;
                                                                                                                                                                                           FF68D74564917510 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
(Fragment).
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Pred. No. 2.9e+03;
1; Mismatches 2;
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                                                                 SEQUENCE.
MEDLINE=96184500; PubMed=8605981;
                                                                                                                             trout cells.";
FEBS Lett. 382:261-264(1996).
PIR; 862893; 862893.
HASSP, QO1853; 1832.
SEQUENCE 21 AA; 2129 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.18;
45.58;
                                                                                                                                                                                                                      33.8%;
Similarity 57.1%;
4; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
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Best Local Similarity
Matches 4; Conserv
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Q9SPV1
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                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Probable profillin LP04 (Fragments)
Orza sativa (Rice)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
   -1- SIMILARITY: Belongs to the allatostatin family.PIR; E47393; E47393.Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
70 kDa cold acclimation-related protein (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 1; Length 13; Pred. No. 1.8e+03; 3; Mismatches 2; Indels
                                                                                                             DB 1, Length 8;
1.8e+06;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actin-binding; Cytoskeleton; Direct protein sequencing; Multigene family.
                                                  3 3 Hydroxyproline (partial).
8 8 Methionine amide.
8 AA; 883 MW; 7D9879CABB477768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0A3022EE0E52C68B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA.
                                                                                                                                                                                                                                                                                        13 AA.
                                                                                                              33.8%; Score 27; DB 100.0%; Pred. No. 1.8 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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13 AA; 1362 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.40,
4; Conservative
                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AVLILOGPP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AYMVIQGEP 13
                                                                                                                                                                            8 GPPY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                           1 GPPY 4
                                                                                                                                                                                                                                                                                      PROX_ORYSA
                                                  MOD_RES
MOD_RES
SEQUENCE
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SEQUENCE
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Gaps

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Indels

RESULT 12

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                                                                                                                                                                                                                                                                              0; Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Triticum.
NCBI_TaxID=4565,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                POSTER E., Hattori J., Labbe H., Bedard J., Johnson D., Ouellet T., Miki B.;
Submitted (MRR-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AR13844; AAD56607.1; -.
Hypothetical protein.
NON TER 16
SEQUENCE 16 AA; 1725 MW; 6A4C8A093666240D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92111773; PubMed=1309704;
Pukudome S., Yoshikawa M.;
"Opioid peptides derived from wheat gluten: their isolation and characterization.";
FEBS Lett. 296:107-111(1992).
PIR; S20322; S20322.
SEQUENCE 18 AA; 2120 MW; 09A80A087DE83926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.5%; Score 26; DB 2; Length 18; Best Local Similarity 66.7%; Pred. No. 3.8e+03; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                               Query Match 32.5%; Score 26; DB 2; Length 16; Best Local Similarity 45.5%; Pred. No. 3.3e+03; Matches 5; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
tagging.";
Plant Mol. Biol. 41:45-55(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                            1 EAVLILOGPPY 11
                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE.
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7M1G0
Q7M1G0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gluten.
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Q7M1G0
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Search completed: November 14, 2004, 12:07:36 Job time : 42.0532 secs

10 PYVSWL 15 || || 9 PYGGWL 14

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds (without alignments) 155.938 Million cell updates/sec Run on:

US-09-831-253F-8 80

1 EAVLILQGPPYVSWL 15 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	
1	31	38.8	-	~	847361	T-cell antigen rec
7	31	38.8	-	N	C49048	
m	31	38.8	20	7	565884	translation initia
4	27	33.8		~	E47393	neuropeptide calla
S	27	33.8	1	7	833609	extensin - maize (
9	27	33.8	~	~	S62893	cold-inducible pro
7	26	32.5	-	~	S20322	gluten - wheat
8	25	31.2	_	~	JN0730	hypothetical 1.7K
σ	24	30.0	~	N	A47687	3-dehydroguinate d
10	24	30.0	2	~	PH1729	Ig heavy chain V r
11	24	30.0	7	~	153401	monocyte chemotact
12	23	28.7	1	N	PH1675	Ig heavy chain V r
13	23	28.7	1	~	JU0356	O
14	23	28.7	-	~	PH1676	Ig heavy chain V r
15	23	28.7	-	~	E37390	traA protein - Esc
16	23	28.7	1	N	PH1677	Ig heavy chain V r
17	23	28.7	-	~		Ig heavy chain V r
18	23	28.7	-	7		calotropin DI - mu
19	23	28.7	7	N	PA0027	protein QA100006 -
20	23	28.7	-	~	PH1616	Ig H chain V-D-J r
21	23	28.7	-	7	610	Ig H chain V-D-J r
22	23	28.7	-	~		gene c-fms protein
23	23	28.7	-	7	I51203	n heav
24	23	28.7	П	~	A48354	nonstructural prot
25	23	28.7	7	7	A05313	apolipoprotein A-I
26	23	28.7	~	~	PS0188	superoxide dismuta
27	23	28.7	~	7	PH1731	g heavy
28	23	28.7	7	7	PH1730	
53	23	28.7	7	N	PH1690	b

Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	collagen alpha 1(I	osmotin homolog -	sormatin - sorghum	glutamate-ammonia	Ig heavy chain V r				
PH1688	PH1680	PH1706	PH1679	PH1678	PH1714	PH1721	D56978	F44957	B33174	T03261	PH1689	PH1694	PH1692	PH1695	PH1726
7	2	2	2	2	7	7	2		2		3			3	2
													28.7 23		
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
T-cell antigen receptor VJ junction beta chain - human (Species: Homo sapiens (man) (CiSpecies: Oc-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 (CiSpecies) (CiSpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.8
Best Local Similarity 71.4
Matches 5; Conservative
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5 ILQGPPY 11 :||| || 3 VLQGSPY 9 ò 셤

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment) C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997
C;Accession: C49048
R;Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
B;Lu, J. Immunol. 22, 2413-2448, 1992
A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenil A;Reference number: A49048; MUID: 92387250; PMID: 1387614
A;Accession: C49048
A;Accession: C49048
A;Accession: C49048
A;Accession: C49048
A;Residues: 1-16 <SIO>

Gaps ö Query Match 38.8%; Score 31; DB 2; Length 16; Best Local Similarity 83.3%; Pred. No. 78; Matches 5; Conservative 1; Mismatches 0; Indels

ö

5 ILOGPP 10 :||||| 6 LLQGPP 11 ò 셤

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gluten - wheat
(Species Triticum aestivum (common wheat)
C;Species 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 820322
Fibukudome, S:, Yoshikawa, M:
Fibukudome, S:, Yoshikawa, M:
FEBS Lett. 296, 107-111, 1992
A;Title: Opioid peptides derived from wheat gluten: their isolation and characterization
A;Reference number: 820322; MUID:92111773; PMID:1309704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: phage SPP1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: UN0730
R;Chai, S; Szepan, U; Lueder, G.; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A;Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPP1
A;Reference number: JN0729; MUID:93328123; PMID:8335259
                                                                                                            662893

cold-inducible protein, 70K - rainbow trout (fragment)

cold-inducible protein, 70K - rainbow trout)

cybate: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

cybatesion: 862893

Ryamachita, M.; Ojima, N.; Sakamoto, T.

FBBS Lett. 382, 261-264, 1996

Ayfitle: Induction of proteins in response to cold acclimation of rainbow trout cells.

AyReference number: 862893; WUID:96184500; PMID:8605981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15;
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31.2%; Score 25; DB 2; I
Best Local Similarity 40.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 2; I
Pred. No. 4.7e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical 1.7K protein - phage SPP1
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: protein
A;Residus: 1-21 <YAM>
A;Cross-references: UNIPROT:Q9PRQ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <FUX-
A;Cross-references: UNIPROT:Q7M1G0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 33.8%;
Similarity 57.1%;
4; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A; Molecule type: DNA
A; Residues: 1-15 < CHA>
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GPPY 10
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C; Species: Calliphora vomitoria
C; Species: Calliphora vomitoria
C; Species: Calliphora vomitoria
C; Species: Calliphora vomitoria
C; Accession: E47393
R; Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A; Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequent A; Reference number: A47393; MUID:93211980; PMID:8460157
A; Accession: E47393
A; Accession: E47393
A; Molecule type: protein
A; Residues: 1-8 < DUV>
A; Molecule type: protein
A; Residues: 1-8 < DUV>
A; Accession: Callatostes: MIPROT:P41841
A; Residues: 1-8 < DUV>
A; Molecule type: Brown Callatostes: Molecule files
A; Note: sequence extracted from NCBI backbone (NCBIP:128482)
                                                                                                                                                                        C; Accession: $65884 / Yoorma, H.O.; Thomas, A.A.M. R; Kapperatits, M.A.M.; W.A.M.; M.A.M.; M.A.M.; M.A.M.; M.A.M.; J. Woorma, H.O.; Thomas, A.A.M. A.B. Lett. 365, 47-50, 1995 A; Title: The amino acid sequence of eukaryotic translation initiation factor 1 and its A; Recence number: $65884; MUID:95293122; PMID:7774713 A; Accession: $65884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subsuppose tragment)

C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: 833609
R;Murphy, J.M.; Hood, E.E.
R;Mulcolle: Discussion for extensin size heterogeneity in two maize varieties.
R;Reference number: 833609
R;Mulcolle: Protein
R;Residues: 1-17 < MUR.>
C;Keywords: glycoprotein, hydroxyproline
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                                                                                    translation initiation factor eIF-1 - rabbit (fragments)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb_1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 2; Length 20;
. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.8%; Score 31; DB Best Local Similarity 54.5%; Pred. No. 98; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: protein
A, Residues: 1-9;10-16;17-20 <KAS>
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EEVIQLQGDPF 19
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Best Local Similarity
Matches 4; Conserv
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GPPY 11

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Gaps

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C,Accession: JU0356
R;Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T. Chem. Pharm. Bull. 39, 712-715, 1991
A;Title: Cycloleonutinin, a cyclic peptide from Leonuri fructus.
A;Reference number: JU0356; MUID:91300597; PMID:2070452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig Deavy chain v resuch 1900 mouse)
(Species: Mus musculus (house mouse)
(Spacies: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
(SAccession: PH1675
(SAccession: PH
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Igheavy chain V region (clone NP-6-5) - mouse (fragment)

Igheavy chain V region (clone NP-6-5) - c. precise: Mus musculus (house mouse)

C.Species: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C.Accession: PHI676

R.MCHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
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C;Species: Leonurus artemisia (sagebrush motherwort)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:S69742; NID:g546303; PIDN:AAD14040.1; PID:g4261740
C;Genetics:
A;Gene: IgH-VDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                  Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Exp. Med. 178, 295-307, 1993
A,Title: Antigen-driven B cell differentiation in vivo.
A,Reference number: PH1675, MUID:93301607, PMID:8315385
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Pred. No. 1.2e+03;
1; Mismatches 1;
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80.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 1;
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A;Molecule type: protein
A;Residues: 1-12 <KIN>
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Best Local Similarity
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YTSWV 5
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                                                                                                                                                                                                                                                3-dehydroquinate dehydratase (EC 4.2.1.10) - Amycolatopsis methanolica (fragment)
C;Species: Amycolatopsis methanolica
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47687
R;Euverink, G.J.; Hessels, G.I.; Vrijbloed, J.W.; Coggins, J.R.; Dijkhuizen, L. J. Gen. Microbiol. 138, 2449-2457, 1992
A;Title: Purification and characterization of a dual function 3-dehydroquinate dehydrata A;Reference number: A47687; MUD:93123995; PMID:1479361
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Steenbergen, E.J.; Verhagen, O.J.; van Leeuwen, E.F.; Behrendt, H.; Merle, P.A.; Weste Eur. J. Immunol. 24, 900-908, 1994
A;Title: B precursor acute lymphoblastic leukemia third complementarity-determining regifetal life.
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C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1729
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
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A.Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
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Pred. No. 1.46+03;
Pred. Transhes 2; Indels
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A; Note: sequence extracted from NCBI backbone (NCBIP:122129)
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llarity 60.0%; Pred. No. 1.6e+03;
Conservative 1; Mismatches 1;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-20 <EUV>
A;Cross-references: UNIPROT:P46380
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57.1%;
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Best Local Similarity
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   LILQGPPYVS
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Best Local Similarity
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3 VFVLNGP 9
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traA protein - Escherichia coli plasmid P307 (fragment)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: D7-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: E37390; P90480
R;Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
R;Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
R;Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
A;Title: The sequences of genes bordering oriT in the enterotoxin plasmid P307: comparie
A;Reference number: A37390; MUID:91261994; PMID:2096398
A;Reference number: A37390
A;Molecule type: DNA
A;Residues: 1-13 <GRA>
A;Cross-references: UNIPROT:Q04220; GB:M62986; NID:g150463; PIDN:AAA25525.1; PID:g150468
C;Genetics:
A;Gene: traA
A;Gene: plasmid
C;Superfamily: fimbrial protein
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J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1676
A;Molecule type: mRNA
A;Restdues: 1-13 «MCH>
A;Resperimental B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                   Query Match 28.7%; Score 23; DB 2; Length 13; Best Local Similarity 60.0%; Pred. No. 1.3e+03; Matches 3; Conservative 1; Mismatches 1; Indels
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1 YTSWV 5
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Q8skx9 genista cill
Q7shb6 neurospora
Q76mk9 eurypharynx
Q91593 silene pent
B9b87148 euryphary
Bab87156 euryphary
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Bab89164 euryphary
O9f894 silene pent
O9f898 silene bacc
O9f891 silene sedo
O9f895 silene pent
O9f895 silene pent
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
MEDLINE=92031479; PubMed=1931964;
Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
"Structural and functional correlates of sucrase-alpha-dextrinase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.P., Bidwell S.L., Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
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Eukaryotaim Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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Pred. No. 3.6e+02;
3; Mismatches 3; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
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Last annotation update)
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QBSKXS
QBSKX7
QBSKX7
QBSKX9
Q7SHB6
Q76MK9
QPFS93
BAB87148
BAB87146
BAB87156
QPFS94
QPFS95
QPFS95
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QPFS95
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Biochemistry 30:10399-10408(1991)
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01-MAR-2004 (TrEMBLrel. 26, Creat
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 26, Last
Hypothetical protein (Fragment).
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  Conservative
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Best Local Similarity
Matches 5; Conserv
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STRAIN=17XNL;
PubMed=12368865;
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Q76mm5 euryphary...
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                                                                                          November 14, 2004, 11:57:26; Search time 37.383 Seconds (without alignments) 215.479 Million cell updates/sec
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Compugen Ltd.
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             GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Q8SKX3
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1: uniprot_sprot:*
2: uniprot_trembl:*
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72
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Match Length DB
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seq length: 23
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Gaps

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13 AA; 1484 MW;
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FEBS Lett. 252:83-87(1989)
PIR; S05236; S05236.
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hes 5; Conservative
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NCBI_TaxID=1491;
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                                                                                    Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelli yoelli.";
Nature 419:512-519(2002)
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunhingham D.A., Prelser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janes C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10095,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93020730; PubMed=1404084;
Damjanov A., Damjanov I.;
"Isolation of serine protease from granulated metrial gland cells mice and rats with lectin from Dolichos biflorus.";
J. Reprod. Fertil. 95:679-684(1992).
SEQUENCE 20 AA; 2290 MW; 0A304F61A22C500D CRC64;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X95668; CAA64970.1; -.
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SEQUENCE 9 AA; 1001 MW; 4687A5AB476455B7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Serine protease (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Q79A22;
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etainopterygii, Neopterygii, Teleostai, Anguilliformes,
Eurypharyngidae, Eurypharynx.
NCBI_TaxID=55117;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Excensyme C3 (Fragment).
Clostridium botulinum.
Bacteria, Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
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Toratani S., Yokosawa N., Yokosawa H., Ishii S.I., Oguma K.;
"Immuno-crossreactivity between botulinum neurotoxin type Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 2; Length 22;
Pred. No. 1.6e+03;
1; Mismatches 5; Indels
                                                 Score 26; DB 2; Length 13;
Pred. No. 9.2e+02;
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Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databasee.
EMBL; ABO46477; BAB87140.1; -
GO; GO:0005739; C:mitochondrion; IEA.
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C7C2DF4CFD83A046 CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
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MEDLINE=22967687; Pubmed=12949142;
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45.5%;
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22 AA; 2449 MW;
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SEQUENCE FROM N.A.
STRAIN=W-17, and W-50;
MEDLINE=22779048; PubMed=12897253;
Medline=22779048; PubMed=12897253;
Palaisa K.A., Morgante M., Williams M., Rafalski A.;
"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
EMBL; AY300592; AAP55313.1; -.
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"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1795-1806 (2003).
EMBL; AX300568; AAP55307.1; -.
                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                     Score 25; DB 2; Length 11;
Pred. No. 1.2e+03;
1; Mismatches 0; Indels
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Pred. No. 1.38+03;
1; Mismatches 4; Indels
                                            C6FF9BD6476444D CRC64;
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
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                                          1237 MW;
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Best Local Similarity 54.5
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  PIR; S00616; S00616.

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SEQUENCE 11 AA; 12
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Best Local Similarity
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5 NNPYS 9
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Matches
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"Evolution of the Deep-Sea Gliper Eel Mitochondrial Genomes: Large-Scale Gene Reatrangements Originated Within the Eels.";
Mol. Biol. Evol. 20:1917-1924 (2003).
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                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes,
Eurypharyngidae; Eurypharynx.
WCBI_TaxID=55117,
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Parasporal crystal protein, wax moth-specific (Fragment)
Bactilus thuringiensis.
Bacteria; Firmitottes; Bacillales; Bacilluscae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
                                                      Score 25; DB 2; Length 10;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
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Pred. No. 1.1e+03;
0; Mismatches 3; Indels
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046477; BAB87140.1; -
                            357BFE29C682DB47 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
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62.5%;
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Mitochondrion.
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SEQUENCE 10 AA; 1261 MW;
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Best Local Similarity 62.5
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Best Local Similarity
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STRAIN=A;
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STRAIN=PIS87132;
MEDLINE=22779048; PubMed=12897253;
Palasias K.A., Morgante M., Williams M., Rafalski A.;
Palasias E.A., Morgante M., Williams M., Rafalski A.;
PContrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1795-1806(2003).

EMBL, AY300558; AAP55297.1; -.
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Zea mays (Maize).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Vagnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                     Yamamoto S., Tsuzaki Y., Tougou K., Shinoda S., "Purification and characterization of L-2,4-diaminobutyrate decarboxylase from Acinetobacter calcoaceticus."; J. Gen. Microbiol. 138:1461-1465 (1992).
BIR, B44854; B44864.
SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;
          Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene synthase 2 (Fragment).
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01-0CT-2003 (TrEMBLrel. 25, La
01-0CT-2003 (TrEMBLrel. 25, La
Phytoene synthase 2 (Fragment)
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55.6%;
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54.5%;
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Best Local Similarity 55.v.,
5, Conservative
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Best Local Similarity 54.0%,
Best Local Similarity 54.0%,
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                                             NCBI_TaxID=663;
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PubMed=9538199;
Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;
Nishimura M., Patsuo H., Nakamura A., Sugiyama M.;
Interpretation and characterization of a puromycin-hydrolyzing enzyme from blasticidin S-producing Streptomyces morookaensis.";
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                                                                                                                                                                                                                                                                                                                                                            Streptomyces morookaensis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                            Score 25; DB 2; Length 13; Pred. No. 1.4e+03;
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Pred. No. 1.5e+03;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Puromycin-hydrolyzi\ng enzyme (EC 3.-.-.) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;
                                             9B1E0AA05615C325 CRC64;
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                                                                                                             1; Mismatches
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55.6%;
                                             13 AA; 1449 MW;
                                                                            h 34.7%;
Similarity 54.5%;
6; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel, 24,
EMBL; AY300599; AAP55338.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                            2 SDTVŠKĖPVDI 12
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PYGAWQSPI 13
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RESULT 12 Q9R518

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TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A Bischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Drownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

R And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Widin T.B., Tooshiyuki S., Carninci P., Prange C.,

R Richards S., Worley K.C., Hale S., Garcantor P., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

R Richards S., Worley W., Sodergren B.J., Lu X., Gibbs R.A.,

R Richards S., Worley W., Sodergren B.J., Lu X., Gibbs R.A.,

R Halton B.K., Muzny D.M., Sodergren B.D., Dickson M.C.,

B Hakesbey J., Helton B.K., Touchman J.W., Green B.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

K Tarywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                            Palaisa K.A., Morgante M., Williams M., Rafalski A.;
"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1795-1806(2003).
EMBL; AY300550; AAP55289.1; -.
NON TER 1 18 18
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Entaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Pred. No. 2e+03;
1; Mismatches 4; Indels
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EMBL; BC002154; AAH02154.1; -.
MGD; MGI:104574; Ptpri;
SEQUENCE 22 AA: 2559 MW; 34843A007475028A CRC64;
                                                                                                                                                                                                                       SEQUENCE 18 AA; 2000 MW; 8ECB4B9056459674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 AA
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                                        STRAIN=P1221785;
MEDLINE=22779048; PubMed=12897253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Ptprj; Synonyms=AW125753;
Mus musculus (Mouse)
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54.5%;
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Matches 4; Conservative
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SEQUENCE FROM N.A.
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Search completed: November 14, 2004, 12:07:34 Job time : 37.383 secs

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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION TORNATION:
RELEASTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 36,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
TENTORIA 14 amino acids
US-08-967-727-6
US-09-064-964-2
US-08-037-220D-6
US-09-64-174-2
US-09-53-850-6
US-09-579-197-6
US-09-579-197-6
US-09-454-204A-66
US-09-454-204A-66
US-09-454-204A-66
US-09-149-476-722
US-08-977-787-7
US-08-974-2284-2284-228
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STRET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
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Dower, Worlliam J.
Barrett, Ronald W.
Gurla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramaniam, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/08764640
Patent No. 5869451
Patent No. 5869451
Patent No. 5869451 5837683
GENERAL INFORMATION:
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Podduturi, Surekha
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TYPE: amino acid
STRANDEDNESS:
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     APPLICANT:
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US-08-764-640-39
        Sequence 216, 1
Sequence 39, Ag
Sequence 39, Ap
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- 42.633 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-973-225-316
US-09-244-39
US-09-549-090-216
US-09-549-090-216
US-09-812-230A-39
US-09-812-230A-37
US-08-856-663-12
US-08-973-225-37
US-08-973-225-37
US-09-244-298A-37
US-09-244-298A-37
US-09-516-704-37
US-09-516-704-37
US-09-161-878-19
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US-08-461-566-6
US-08-142-368A-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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80
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                     Run on:
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No.
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APPLICANT:
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                                                       Gaps
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                 DB 2; Length 14; 48;
                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: TEM PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                   Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS '
THOMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELEDOMYNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDENESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                   Score 33;
Pred. No.
                                                                                                                                                                                                                  Sequence 39, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
BETTER, William J.
CWitzla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-973-225-216
; Sequence 216, Application US/08973225A
; Sequence 106, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acide
                 41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 6; Conservative
                                                     6; Conservative
                                                                                                                  3 LVGPSLMSWL 12
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                                                                                           6 LQGPPYVSWL 15
               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                     RESULT 2
US-08-973-225-39
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwila, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Pecer J.
APPLICANT: Schatz, Pecer J.
APPLICANT: Handren, Rajerrom, Christopher R.
APPLICANT: Handren, Richard W.
APPLICANT: Hendren, Richard W.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                          THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
COMPUTER TABLOABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
COMPUTER: TBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                   Schatz, Peter J.

Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PETIDES AND COMPOUNDS THROMBOPOLETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.2%; Score 33; DB 3; 60.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-08-973-225-216
                                                                                                                                                                                                                                                                                                                                            CITY: Research Triangle Park STATE: NC
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-244-298A-39
'Sequence 39, Application US/09244298A
'Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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Best Local Similarity
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Gaps

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                                                                                                                                                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 3;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hrubiec, Robert T.
REGIGTRATION NUMBER: 36.392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/973,225
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 99-244-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.(
CIȚY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Matthaskis, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/09549090
Patent No. 6465430
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
                                                                                                                                                                               LENGTH: 14 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LVGPSLMSWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LOGPPYVSWL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 27709
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Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC.1996
CLASSIFICATION: 514
ATTOMREY/AGENT INPORMATION:
NAME: HTLDIEC: Robert T.
REGISTRATION NUMBER: BK3281
TELECOMMUNICATION INFORMATION:
39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.O. Box 13398
                      Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIPICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.(
CITY: Research Triangle Park
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                      TREET: Five היסיים Triangle Park
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LVGPSLMSWL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-244-298A-39
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RESULT 8
US-09-832-230A-39
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEFTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPER: FLOPRY
MEDIUM TYPER: FLOPRY disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATCHITIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION NUMBER: US 08/973,225
FILING DATE: CURNOWN:
APPLICATION NUMBER: US 08/973,225
FILING DATE: CURNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: HINDIGC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
                                                                                      Score 33; DB 4; Length 14;
Pred. No. 48;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-549-090-216
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-549-090-39
                                                                                                                                                                                                                                                                             US-09-549-090-216
Sequence 216, Application US/09549090
Patent No. 6465430
GENERAL INFORMATION:
BATTEL, Romald W.
Cyirla, Steven E.
Duffin, David J.
Haselden, Sherril S.
Haselden, Sherril S.
Schatz, Peter J.
Schatz, Pater J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.C.
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 14 amino acids
                                                                                      Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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                                                                                                                                                                 6 LOGPPYVSWL 15
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Best Local Similarity
Matches 6; Conserv
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Sequence 39, Application US/09832330A
Sequence 39, Application US/09832230A
Batent No. 6506362
GENERAL INFORMATION:
APPLICANT: Dower, William J. et al
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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Sequence 67, Application US/09428082B
Fatent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: CHESTHAM, JANET C.
APPLICANT: HOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 4; Length 14;
Pred. No. 48;
1; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                      MEDITURE Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/832,230A
FILING DATE: 10-Apr-2001
CLASSIFICATION: «Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GlaxO Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hrubiec, Robert T.
REGISTRATION UNDRER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 39: US-09-832-230A-39
                                                                                                                                                                                                                                           CITY: Research Triangle Park STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14 amino acids
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SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
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Best Local Similarity 60.0
Matches 6; Conservative
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... FLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SUCRESCE: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcon
STREET: Five "
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.0%; Score 32; DB 2; Length 14; Best Local Similarity 55.6%; Pred. No. 70; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTONREY/AGENT INPOMENTION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REGISTRATION NUMBER: 36,392
REPERENCE/POCKET NUMBER: 36,392
RELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION OF SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                              Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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APPLICANT: Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrett, Ronald W. Cwirla, Steven E. Duffin, David J. Gates, Christian
                                                                                                                                                                                                                                                                       STREET: Glaxo Wellcome STREET: Five Moore Drive, P.O. CITY: Research Triangle Park STATE: NC COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                   Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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   GENERAL INFORMATION:
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                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                           Sequence 12, Application US/08856663
Fatent No. 5849558
GENERAL INFORMATION:
APPLICANT: CHANG, ZHIYUH
TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE TITLE OF INVENTION: PSPGI RESTRICTION ENDONUCLEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSER: New England Biolabs, Inc.
STREET: 32 Tozer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 11;
                                                         DB 4; Length 14;
                                                                                            3; Indels
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                                                       Score 33; DB 4; Pred. No. 48; 1; Mismatches
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Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 01915
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSTENG Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,663
FILING DATE: 15-MAY-1997
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE US-09-428-082B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08764640; Patent No. 5869451; Patent No. 5869451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECONAUNICATION INFORMATION:
TELEPHONE: 978-927-5054
TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30901
                                                     Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams, Gregory REGISTRATION NUMBER: 309 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                 6 LOGPPYVSWL 15
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US-08-764-640-37
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Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO
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Pred. No. 70;
                                                                                                                                                                                                                                                                                                                    3; Indels
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APPLICATION NUMBER: US/09/516,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Garatz, Peter J.
Balagubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagstrom, Christopher R
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
STRANDEDNESS:
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11-DEC-1996
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6
Best Local Similarity 55.6
                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-09-244-298A-37
                                                                                                                                                                                                                                                                                                                                                       7 OGPPYVSWL 15
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                                                                                                                                                                                                                      linear
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US-09-516-704-37
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                                                                         Query Match 40.0%; Score 32; DB 3; Length 14; Best Local Similarity 55.6%; Pred. No. 70; Matches 5; Conservative 1; Mismatches 3; Indels
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                 P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schatz, Peter J.
Balasubramantan, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-973-225-37
                                                CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/244,298A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
             ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Five Moore Drive, P. CIIY: Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 OGPPYVSWL 15
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Search completed: November 14, 2004, 13:18:38 Job time: 23.3333 secs
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Barrett, Ronald W.
Cwila, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheast, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STRIE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SONTWARE: Patentin Release #1.0, Version #1.30
                                                                               Query Match
40.0%; Score 32; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.0%; Score 32; DB 4; Length 14; Best Local Similarity 55.6%; Pred. No. 70; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY CURRENT US 08/973,225
FILING DATE: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: HINDIEC, ROBERT T.
REGISTRATION UNMERR: 9K3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: «Unknown»
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-549-090-37
;
US-09-516-704-37
                                                                                                                                                                                                                                                                                                                          ; Sequence 37, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 OGPPYVSWL 15
                                                                                                                                                                     7 QGPPYVSWL 15
                                                                                                                                                                                                                3 OGPTLTAWL 11
                                                                                                                                                                                                                                                                                                        US-09-549-090-37
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3 OGPTLTAWL 11

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2004, 13:32:33 ; Search time 22.5 Seconds (without alignments) 59.868 Million cell updates/sec Run on:

US-09-831-253F-7 72

1 SNPYSAFQVDITID 14 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2096 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 14 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	parasporal crystal	L-2,4-diaminobutyr	glandular kallikre	vespakinin M - hor	hypothetical prote	glycoprotein H-a -	ribosomal protein	unidentified 85K p	enamelin i - bovin	Ig heavy chain CDR	MUC1 enhancer bind	ribosomal protein	R-phycoerythrin ga	proteochondoitin c	very late antigen-	neuropeptide calla	Ig heavy chain CRD	amine oxidase (cop	Ig kappa-1 chain J	avenin alpha-2 - o	Pax-QNR, long form	prealbumin - weste	MHC class I histoc	protein QA100052 -	Ig heavy chain C r	ornithine decarbox	NADH2 dehydrogenas	H-hyosophorin - Ja	T-cell receptor be
	ID	800616	B44854	A54326	A61360	PS0371	A40795	836899	PC2369	S10784	PT0229	A59018	836898	G22565	PT0077	A28018	D47393	PT0250	S70344	B20907	829209	B56884	I49404	JQ0914	PA0050	C39111 ,	B33710	PS0275	A34243	PH0771
	DB	2	7	~	7	7	7	~	~	7	7	~	~	~	~	0	~	7	7	N	0	~	~	~	N	~	N	N	~	7
	Length	11	14	13	12	14	11	12	13	σ	11	14	თ	13	14	14	<b>8</b> 0	11	12	13	14	14	œ	Q	10	10	10	11	11	12
de	Query Match	34.7	34.7	31.9	30.6	30.6	29.5	29.5	29.5	27.8	27.8	27.8	26.4	26.4	26.4	26.4	25.0	25.0	25.0	25.0	S	25.0	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6
	Score	25	25	23	22	22	21	21	21	20	20	20	19	19	19	19	18	18	18	18	18	18	17	17	17	17	17	17	17	17
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T-cell receptor be T-cell receptor be T-cell and and a second a seco	tubulin alpha-chai Ig H chain V-D-J r	bradykinin-like pe alcohol dehydrogen	T-cell receptor be ermG leader peptid phyllokinin - Rohd	T-cell receptor be Ig heavy chain CRD vespakinin X - hor	spore proteinase g osteoclast functio
PH1462 PH1457 S47361	54/361 S65612 PH1615 S07768	A61362 S71919	PH0916 A26930 A61365	S26546 PT0257 A61359	A61288 A33660
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## ALIGNMENTS

 RESULT 1 S00616
 parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleriae N'Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C.Species: Bacillus thuringiensis
C;bate: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_cnange 09-Jul-2004 C;Accession: S00616
R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M. FRBS Lett. 232. 249-251. 1988
A; Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxi
A.Reference number: S00615
A; Molecule type: protein
A; Residues: 1-11 < CHE>
A;Cross-references: UNIPROT:Q7M154
C; Comment: This toxin is effective against the larvae of Galleria melonella (greater wax
C,Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin
Query Match 34.7%; Score 25; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SNPYS 5

B44854

L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - Vibrio alginolyticus (fragment)
C;Species: Vibrio alginolyticus
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004
C;Accession: B44854; B41817
C;Accession: B44854; B41817
J. Gen. Microbiol. 138, 1461-1465, 1992
A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from Ac A;Reference number: A44854; MUD:92381494; PMID:1512577
A;References number: A44854
A;Molecule type: protein
A;Residues: 1-14 < YAM>
A;Cross-references: UNIPROT:09R518
A;Cross-references: UNIPROT:09R518
A;Cross-reference extracted from NCBI backbone (NCBIP:112332)
C;Keywords: carbon-carbon lyase; carboxy-lyase B44854

Query Match 34.7%; Score 25; DB 2; Length 14; Best Local Similarity 55.6%; Pred. No. 2.6e+02; Matches 5; Conservative 2; Mismatches 2; Indels 5 SAFQVDITI 13 :||:|| | 2 TAFEVDSNI 10 à g

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Gaps

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Gaps

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Indels

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Mismatches

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3; Conservative

Matches

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glycoprotein H-a - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Lo-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-1993
C;Accession: A40795
R;Christie, D.L.; Batchelor, D.C.; Palmer, D.J.
J;Biol. Chem. 266, 15679-15683, 1991
A;Ttle: Identification of kex2-related proteases in chromaffin granules by partial aminc A;Reference number: A40795; MUID:91340701; PMID:1874725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S36699
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 311, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact A;Reference number: S36887; MUID:94009653; PMID:8405418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC2369
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
(5)Species: Bacillus cereus
(5)Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
(5)Accession: PC2369
R Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-215, 1955
A;Title: Identification of DNA-binding proteins changed after induction of sporulation in A;Reference number: PC2369; MUID:95218265; PMID:7766022
A;Accession: PC2369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosomal protein S6 - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
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Pred. No. 1.1e+03;
3; Mismatches 4;
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Pred. No. 1.2e+03;
0; Mismatches 4
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A Molecule type: protein
A Readleus: 1-12 < CHA>
C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <MAS-
A;Cross-references: UNIPROT:Q7M0L4
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Best Local Similarity 50.0%;
Matches 4; Conservative
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A/Molecule type: protein
A/Residues: 1-11 <CHR>
C/Keywords: glycoprotein
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nes 3; Conserv
7 FQVDIT 12
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Matches 3;
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PS0371

PS0371

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PS0371

C;Ppothetical protein (psaC region) - Synechococcus sp. (fragment)

C;Species: Synechococcus sp.

C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999

C;Accession: PS0371

R;Rhial, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.

Gene 112, 123-128, 1992

A;Title: The psaC genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning an A;Reference number: JS0694; MUID:92201692; PMID:1551590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Vespa mandarinia
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A61360
R;Kishimuxa, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ven
A;Reference number: A61360; MUID:77114342; PMID:1017116
                                               glandular kallikrein-1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A54326
R;Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J. Mol. Cell. Endocrinol. 76, 181-190, 1991
A;Title: Identification and androgen-regulated expression of two major human glandular A;Reference number: A54326; MUID:92324494; PMID:1726490
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                                                                                                                                                                                                                                                                                  A;Accession: A54326
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-13 < RE>
A;Experimental source: prostate
A;Note: sequence extracted from NCBI backbone (NCBIP:108060)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.9%; Score 23; DB 2; Length 13; Best Local Similarity 80.0%; Pred. No. 5.5e+02; Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Superfamily: unassigned animal peptides
C.Keywords: hydroxyproline; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12;
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42.9%; Pred. No. 7.7e+02;
tive 3; Mismatches 1;
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A61360
vespakinin M - hornet (Vespa mandarinia)
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Best Local Similarity 42.5
Matches 3; Conservative
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Molecule type: protein
Residues: 1-12 <KIS>
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Best Local Similarity
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A; Residues: 1-14 <RHI>
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RESULT 9

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Tibosomal protein S8 - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Species: S34698
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact A;Reference number: S36898
A;Reference number: S36898
A;Reference number: S36898
A;Reference protein
A;Reference protein
A;Residues: 1-9 cOHA>
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteochondoitin core protein - rat (fragment)
proteochondoitin core protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: PT0077
R;Marcum, -1.1, Thompson, M.A.
Biochem. Biophys. Res. Commun. 175, 706-712, 1991
A;Title: The amino-terminal region of a proteochondroitin core protein, secreted by aortion human bone.
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                                                                                                                                                                                     Gaps
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llarity 42.9%; Pred. No. 2.8e+05;
Conservative 3; Mismatches 1;
       A;Note: 3-Val was also found
C;Keywords: DNA binding; heterodimer
                                                                                                             Query Match
Best Local Similarity 33.3%;
Matches 3; Conservative
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C;Species: Homo sapiens (man)
C;Species: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C;Accession: A59018
R;Abe, M:; Smith, C.J.; Larson, C.J.
submitted to the Protein Sequence Database, May 1998
A;Description: Involvement of "Ku-like" proteins in the transcription of MUCI/DF3, a bre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S10784
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A;Reference number: S10780; MUD:90336641; PMID:2379503
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0229
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R;Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
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C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0;
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A;Residues: 1-14 <ABE>
A;Experimental source: breast cancer cell line MCF-7
29.2%; Score 21; DB 2; I
50.0%; Pred. No. 1.3e+03;
iive 2; Mismatches 1;
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A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: protein
A,Residues: 1-9 <STR>
A,Cross-references: UNIPROT:Q7M2M7
C,Keywords: enamel; phosphoprotein
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
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RESULT 11

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A;Molecule type: protein
A;Residues: 1-14 <MAR>
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
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A; Status: preliminary
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RESULT 15
A28018
very late antigen-1 alpha chain - human (fragment)
NyAlternate names: VLA-1 alpha chain
NyAlternate names: VLA-1 alpha chain
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1889 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994
C;Date: 30-Jun-1889 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994
C;Accession: A28018
R;Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A;Title: The very late antigen family of heterodimers is part of a superfamily of molecularycence number: A94151; MUID:87204112; PMID:3033641
A;Reference number: A94151; MUID:87204112; PMID:3033641
A;Reference type: protein
A;Residues: 1-14 cTAK>
C;Keywords: duplication; heterodimer; membrane protein

Query Match 26.4%; Score 19; DB 2; Length 14; Best Local Similarity 60.0%; Pred. No. 3.2e+03; Matches 3; Conservative 1; Mismatches 1; Indels

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Search completed: November 14, 2004, 13:45:47 Job time: 22.5 secs

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AAB88035 AAR21773 AAY99308 AAY3520 AAR35820 AAR35820 AAR36445 AAB6648 AAB6648 ABR17659 ABR17659 ABR17659 ABR17659 ABR1765134 ABR1765134 ABR1765134 ABR1765134 ABR1765134	ALIGNMENTS	14 AA.		inhihitom	r innibitory per transforming g ollagen synthes adation inhibit					5.	TECNOLOGICO NAVARRA e Sagastibelza JJ,		g of iseas recep	Spanish.	with (TGF) factor betal (TGF) factor f
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulati; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                             Human BLyS binding scFv VH CDR3 SEQ ID 3097.
ABP47086 standard; peptide; 10
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21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                           ABP47086;
                                                                                                                                                                                                                                                                                                                                                                                              (CAMB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial anino acid sequences identical, or similar, with those of TGF-bl and/or its receptors Peptides AAY92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or
                                                                                                                                                                                                                                                                       Hepatotropic, antagonist, transforming growth factor betal, IGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
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                    Score 72; DB 3; Length 14;
Pred. No. 1.2e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                              Transforming growth factor inhibitory peptide P145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 31; 86pp; Spanish.
                                                                                                                                                                  AAY93099 standard; peptide; 14 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease, specifically cirrhosis
                     ch
1 Similarity 100.0%;
14; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                    98ES-00002465
                                                                           1 SNPYSAFQVDITID 14
                                                                                                1 SNPYSAFQVDITID 14
                                                                                                                                                                                                                      08-NOV-2000 (first entry)
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                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14 AA;
Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                     WO200031135-A1
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2000
                                                                                                                                                                                             AAY93099;
                        Query Match
                                                  Matches
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Hilbert

Choi GH, Vaughan T,

Barash SC,

CAMBRIDGE ANTIBODY TECHNOLOGY.

2001US-0276248P. 2001US-0277379P.

2000US-0212210P. 2000US-0240816P.

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the Lymphocyte Stimulator (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell controlleration and differentiation. The antibodies G the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antibheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be amountained to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP41228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                             Claim 2; Page 3114; 3148pp; English.
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SPYDAFDI 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 AA;
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RESULT 4 ADG97913

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Gaps

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100.0%; Score 72; DB 3; Length 14; 100.0%; Pred. No. 1.2e-06; Live 0; Mismatches 0; Indels

SNPYSAFQVDITID 14 1 SNPYSAFOVDITID 14

RESULT 3

14; Conservative

Matches

Local Similarity

Query Match

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Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                  antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                               scFV VHCDR3 peptide that immunospecifically binds BLyS SeqID 3097.
                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 3097; 394pp; English.
ADG97913 standard, peptide, 10
                                                                                                                                                                                                                     14-NOV-2002; 2002WO-US036496.
                                                                                                                                                                                                                                          16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                           11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                      WPI; 2003-505530/47.
                                                                                                                                                                         WO2003055979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                    Unidentified
                                                                                                                                                                                                10-JUL-2003
                      ADG97913;
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Vaughan TJ, Hilbert D;

Choi GH,

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13434 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single cain antibody molecules (screy) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The freament invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As uch, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaema, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antialthritic, neuroprotective, activities such as antiartheumatic, antialthritic, neuroprotective, caliniting manalogy, they can be described and cytostatic. This peptide sequence is a single chain antibody variable heavy CDR3 peptide that immunospecifically binds BLyS of the invention.

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                        Gaps
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  Length 10;
                      Indels
Score 28; DB 7; Le:
Pred. No. 1.8e+02;
2; Mismatches 2;
 38.98;
           50.08;
                       4; Conservative
        Best Local Similarity
Matches 4; Conserv
 Query Match
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SPYDAFDI 10 2 NPYSAFQV 9

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AAB10012 standard; protein; 13 AA. RESULT 5
AAB10012
ID AAB10

AAB86092 standard; peptide; 13 AA.

AAB86092;

AABB6092 ID AABE XX AC AABE RESULT 6

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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal seample with at least two different monoclonal antibodies (WAD) for their fragments or derivatives) or aptamers (collectivels) (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of formation of a complex (C) between (I) and the corresponding antigen of (Ag). The first and second (I) bind to epitopes of different antigens (C) in at least some mammals, and have either: (i) their native structure; or infected or immunized with (A), or its extract. Jysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, aparticularly of the genera Helicobacter, contexpensive and easily standardizable diagnosis, despite possible contexpensive and easily standardizable diagnosis, despite possible contexpensive and easily standardizable beta-urease-binding contexpensive contexpensive and a fragment of a H. Pylori H. Pylori Contexpensive and a fragment of a H. Pylori Contexpensive contexpensive and a fragment of a H. Pylori Contexpensive contexp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a fecal sample with two binding reagents for
                                                                                                                                           Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heavy chain; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody heavy chain complementarity determining region CDR3 which is used to illustrate the method of the invention
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    pylori beta-urease-binding antibody heavy chain CDR3 protein #2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigens that survive intestinal passage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 22; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                99WO-EP008212.
                                                                                                                                                                                                                                                                                                                                                                                                                                              98EP-00120517
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                                              01-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-365747/31.
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                                                                                                                                                                                                 CDR; beta-urease.
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                                                                                                                                                                                                                                                                                                WO200026671-A1
                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1999;
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06-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reiter C,
AAB10012;
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This invention describes a novel method for detecting, in a mammal, infection by an acid-resistant microorganism (A) which comprises reacting a fecal sample with: (I) a receptor (R) such that a complex is formed with (A) or (I); two different R so that a three-part complex is formed with Ag, and the formation of a complex detected. R are specific for an Ag which, after passage through the intestines, at least in some mammals, retains a native (or corresponding) structure against which the mammal produces antibodies (when immunized or infected with (A), or its extracts, lysates or derived proteins (or fragments) or synthetic peptides). The products of the invention have antibacterial activity. The method is used to diagnose infection by Helicobacter, C ampylobacter or Mycobacterium, particularly H, pylori (most preferred), the hepatica, C. jejuni and M. tuberculosis, and also to monitor the progress of treatment. Receptors, particularly antibodies, directed against Ag can be used therapeutically for treatment of infections. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection. This sequence represents a complementarity determining region (CDR) from an antibody generated against a Helicobacter pylori antigen (catalase or beta-urease) which is used to illustrate the method of the
infection; acid-resistant microorganism; fecal; antibody; diagnosis;
antibacterial; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting infections by acid-resistant microorganisms, particularly diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method requires only one R to provide a reasonably secure diagnosis (although use of two R improves sensitivity), so is relatively inexpensive and more easily standardized. Also it is direct, non-invasive, suitable for automation and may indicate the stage of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-dependant Clp proteinase (clpL) epitopic peptide #SEQ ID 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 17; 89pp; German.
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                                                                                                                                                                                                                                                                                12-OCT-1999; 99EP-00120351.
16-MAR-2000; 2000EP-00105592.
31-MAR-2000; 2000EP-00107028.
10-MAY-2000; 2000EP-00110110.
                                                                                                                                                                                                                                12-OCT-2000; 2000WO-EP010058.
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Matches 5; Conservative
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                                                                                                                          WO200127613-A2
                                                                          Unidentified
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                                                                                                                                                                             19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid-resistant microorganism (A), in a mammal, using immunochromatography. The method is used to diagnose infection by an acid resistant microorganism (A), in a mammal, using immunochromatography. The method is used to diagnose infection by an acid campylobacter or Mycobacterium, particularly H. pylori (most preferred), H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple, inexpensive and non-invasive, and may indicate the stage of infection. A test strip used in the method may indicate the stage of infection. A present in the sample and only a single receptor provides a reasonably secure diagnosis, with specificity and selectivity improved by detecting several epitopes (of catalase) or different antigens (catalase and betaurease). The method can be automated. This sequence represents a urease). The method can be automated (CDR) from an antibody raised against the H. pylori catalase or beta-urease antigen which is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting infections by acid-resistant microorganisms, particularly for diagnosing Helicobacter pylori, comprises immunochromatographic detection of antigen in feces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
                                                                                                                     Catalase; beta-urease; antibody; antigen; detection; infection; epitope; acid-resistant microorganism; complementarity determining region; CDR; feces; heavy chain; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for detecting infection by an
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                                                                        H. pylori beta-urease derived antibody light chain CDR3 #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dehnert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB86060 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 27; 90pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1999; 99EP-00120351.
16-WAR-2000; 2000EP-00105592.
31-WAR-2000; 2000EP-00107028.
30-WAY-2000; 2000EP-00110110.
                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000; 2000WO-EP010057
                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282086/29.
N-PSDB; AAF88119.
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                                                                                                                                                                                                                                                                                WO200127612-A2.
                                                                                                                                                                                                                             Unidentified.
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                        17-JUL-2001
                                                                                                                                                                                                                                                                                                                                  19-APR-2001
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for

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Haindl

Mueller H,

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Gaps

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Query Match

Matches

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AAB86060;

RESULT 7
AAB86060
ID AAB8
XX
AC AAB8
XX
DT 17-J
XX
DE H. P
XX
KW Heav

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

Human BLyS binding scFv VH CDR3 SEQ ID 2839.

(first entry)

19-AUG-2002

ABP46828;

ABP46828 standard; peptide; 11 AA.

RESULT 9 ABP46828

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New crystallized recombinant polypeptides and polynucleotides encoding them, useful in developing antimicrobial agents for treating or preventing infection or contamination, or for inducing an immunological
     Antimicrobial; immunostimulant; gene therapy;
ATP-dependent Clp proteinase; proline dipeptidase; chorismate mutase;
aminotransferase; serine hydroxymethyltransferase;
O-acetyleerine sulfhydrolase B; translocase; tRNA methyltransferase;
3-dehydroquinate synthase.
                                                                                                                                                                                                                                                                  Dharamsi A, Vedadi M, Alam MZ,
Domagala M, Kanagarajah D, Li
Ng I, Pinder B, Sheldrick B, V
                                                                                                                                                 2001US-0324139P.
2001US-0325333P.
2001US-0325836P.
2001US-0338235P.
                                                                                                                                                                                      2001US-0343758P.
2001US-0340531P.
2001US-0340945P.
2001US-0333281P.
                                                                                                                        20-SEP-2002; 2002WO-CA001426
                                                                                                                                                                                                                              2002US-0399926P
                                                                                                                                                                                                                                                 (AFFI-) AFFINIUM PHARM INC.
                                                               Staphylococcus aureus,
                                                                                                                                                                                                                                                                                                                WPI; 2003-371794/35.
                                                                                  WO2003025005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 AA;
                                                                                                                                                                                                 26-OCT-2001;
30-OCT-2001;
06-NOV-2001;
                                                                                                                                                                                                                                                           Edwards A, D
                                                                                                                                                                    28-SEP-2001;
25-OCT-2001;
                                                                                                                                                                                        25-OCT-2001;
                                                                                                                                                             27-SEP-2001;
                                                                                                                                                  21-SEP-2001
                                                                                                    27-MAR-2003
                                                                                                                                                                                                                                                                              Canadien V,
Nethery K,
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Vaughan T, Hilbert D;

Choi GH,

Ruben SM, Barash SC,

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

17-0CT-2000; 2000US-0240816P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P. 25-MAY-2001; 2001US-0293499P.

, Awrey D, Beattie B; i Q, Mansoury K, Necakov S; Vallee F, Viola C;

15-JUN-2001; 2001WO-US019110.

16-JUN-2000;

WO200202641-A1

10-JAN-2002.

Homo sapiens.

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The invention relates to a novel crystallists recommuning purpopertice of the invention has at least one biological activity of ATP-dependent Clp proteinase, proline dipeptidase, chorismate mutase homology branched-chain amino acid aminotransferase or serine mutase homology branched-chain amino acid aminotransferase chos staines by the construction of the machyltransferase from Staphylococcus aureus, O-acetylserine sulfhydrolase B from Escherichia coli, preprotein translocase secretion by protein or RNA methyltransferase from Helicobacter pylori, or 3-dehydroquinate synthase from Streptococcus unseful in antisense therapy, cholypeptides of the invention are useful in antisense therapy, as diagnostic agents to detect the presence of the target DNA or RNA sequences to which the specifically bind, and in producing recombinant polypeptides. The polypeptides are useful for producing specific antibodies which modulate the action of the polypeptides, and in identifying compounds which modulate the action of the polypeptides and in the treatment in munological response. Sequences given in ADH48561-ADH48641 represent polypeptides and polymelectides that are identified in the represent polypeptides and polymelectides that are identified in the crops of the invention as microbial target sequences.
                                                                                                                      invention relates to a novel crystallised recombinant polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the proteins, and primers used for their amplification
Disclosure; SEQ ID NO 12; 172pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 3062; 3148pp; English.
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nes 4; Conserv
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8
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Gaps ;

Score 27; DB 7; Length 10; Pred. No. 2.8e+02; 0; Mismatches 4; Indels

37.5%; 55.6%;

Query Match Best Local Similarity

5; Conservative

Matches

2 NPYSVILFD 10

2 NPYSAFOVD 10

ઠે 셤 endothelial cell binding protein; ECBP; anti-tumour; cytostatic; vasotropic; antipsoriatic; dermatological; ophthalmological; antiathritic; vulnerary; antiulcer; antinflammatory; antibacterial; gynaecological; anglogenesis.

01-NOV-2002; 2002WO-US035258.

WO2003037172-A2.

Synthetic.

08-MAY-2003

01-NOV-2001; 2001US-0334822P.

(GPCB-) GPC BIOTECH INC

Endothelial cell binding peptide SEQ ID NO:177.

(first entry)

18-DEC-2003

ADC44449;

ADC44449 standard; peptide; 12 AA.

9

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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13434 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (screw) derived, preferably, it refers to single heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodises in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and cytostatic. This peptide sequence is a single chain antibody variable heavy CDR3 peptide that immunospecifically binds BLyS of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                     antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AlDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                             BCFV VHCDR3 peptide that immunospecifically binds BLyS SeqID 2839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH, Vaughan TJ, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 2839; 394pp; English.
                                        ADG97655 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2002; 2002WO-US036496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-2001; 2001US-0331469P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN. GENOME SCI INC.
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-505530/47.
                                                                                                                                                                                                                                                                                                                                                                  WO2003055979-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 AA;
                                                                                                                      11-MAR-2004
                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-2003
                                                                                ADG97655;
RESULT 10
                     ADG97655
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The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell peptide of the invention has anticulation to the invention by sequences. A peptide of the invention has anticulation typostatic, vasotropic, antiarthritic, dermatological, antidiabetic, antiarthritic, vulnerary, antiulcer, cophthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer, cophthalmological, confidencial, and gynaecological activity. The peptide is useful for promoting, reducing the proliferation and/or migration of the preferably the peptide, to promote proliferation and/or migration of the treated cells, and for reducing or promoting angiogenesis, by treating the cells with an ECBP antagonist, which is preferably the peptide of the invention is also useful for manufacturing a medicament for promoting angiogenesis, by dimixing an enderming antagonist to promote or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis. ECBP sequences are useful for promoting or reducing angiogenesis. ECBP sequences are useful to alter the infectivity spectrum of a viral particle. The present sequence represents an ECBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel synthetic or recombinant polypeptide useful for promoting, reducir proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Tsaioun K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID NO 177; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Morris AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR67117 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Lamphere L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-482072/45.
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Best Local Similarity
Matches 5; Conserv
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30-JUN-1995
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AAR67117
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Gaps

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Score 27; DB 7; Length 11; Pred. No. 3.1e+02; 1; Mismatches 2; Indels

37.5%; 57.1%;

Query Match Best Local Similarity

4; Conservative

Matches

5 PYDAFDI 11

RESULT 11 ADC44449

3 PYSAFQV 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67114-17 are anti-inflammatory peptides derived from naturally occuring polypeptides that contain proline or proline/cysteine brackets. These peptides are shortened to form fragments that contain one or more interaction sites of interest. AAR6117 is deriv. from fibrinogen gammalinteractions between fibrinogen and its leukocyte receptor Collb/CD18 integrin (Mac-1). The data collected demonstrates that interaction sites possess activity when present in a polypeptide that differs from the native form. Inclusion of conformation-constraining moieties can have desirable effects on an interaction site. (Also see AAR6701-113 and AAR67118-52 for analogues of coher biologically active peptides contg. an interaction site flanked by conformation constraining sps., eg. RGD
                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide homologue or analogue with constrained conformation - has proline residues flanking the interaction site to impart greater, or more stable,
                                               anti-inflammatory peptide; fibrinogen gamma-chain; leukocyte receptor; mimic; interaction site; constrained conformation; inhibitor; CD11b; CD18 integrin; Mac-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                Anti-inflammatory peptide (AIP-FBG1) contg. proline brackets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interaction site flanked by conformation constraining of peptides.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 39; 57pp; English.
                                                                                                                                                                                                                           94WO-US004294.
                                                                                                                                                                                                                                                              93US-00051741,
93US-00143364,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-358186/44.
                                                                                                                                                                                                                                                                                                                                                                      Evans HJ, Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 4; Conserv
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NPWTVFQ 7
                                                                                                                                                                                                                                                                                                                 EVAN/) EVANS H J.
                                                                                                                                                                                                                                                                                                                                   (KINI/) KINI R M.
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                                                                                                                                                       WO9425482-A1
                                                                                                                                                                                                                                                                23-APR-1993;
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                                                                                                                                                                                        10-NOV-1994.
                                                                                                                     Synthetic.
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New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.

Claim 1; Page 48; 60pp; English.

Sidney J;

Sette A, Southwood S, (EPIM-) EPIMMUNE INC.

WPI; 2000-097143/08.

99WO-US012066. 98US-0087192P.

28-MAY-1999; 29-MAY-1998;

02-DEC-1999

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The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an expectation those represented by peptides AAY98812-199339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The comparable binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical focuses the immune response than or equal to 1,000 nM. The pharmaceutical focuses the immune response conversing selected determinants and could therefore be used in cases of chouse to the peptide concaining pharmaceutical include autoimmune concorned using the peptide concaining pharmaceutical include autoimmune concorned using the peptide archritis, multiple sclerosis, and myasthenia cresponses rheumatoid archritis, multiple sclerosis, and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides.

Concor, hypersensitivities. The peptide epitopes can be used to enhance immune response against other immunogens administered with the peptides cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, carcinal cancer, hepatitis B, hepatitis C, AIDS, renal carciname, carcinal cancer, hepatitis B, hepatitis C, AIDS, renal carciname, carciname, cancer, hepatitis B, hepatitis C, AIDS, renal carciname, carciname, cancer, hepatitis B, hepatitis C, AIDS, renal carciname, carciname, cancer, hepatitis B, hepatitis C, AIDS, renal carciname, carciname, individuals will be at substantial risk of developing chronic infection.

The selection of appropriate T and B cell epitopes should allow the epitopes of pathogens which are characterized by high sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitopes of pathogens which are characterized by high sequence variability such as HIV, HCV and Malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 27; DB 3; Length 14; 50.0%; Pred. No. 4.2e+02; ive 2; Mismatches 3; Indels
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Best Local Similarity
Matches 5; Conserva
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immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allargy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria. Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;

Unidentified

HLA class II binding antigen epitope peptide #495.

07-AUG-2000 (first entry)

AAY99306;

AAY99306 standard; peptide; 14 AA.

RESULT 13

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The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitode selected from those represented by peptides AAY98812-99339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The class DR molecules at an IC-50 of less than or equal to 1,000 mM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be cromic viral diseases and cancer. Examples of diseases that can be containing pharmaceutical include autoimmune confiseases (rheumatoid arthritis, multiple sclerosis, and myssthania gravis), allograft rejection, allergies, lyme disease, hepatitis, postcrost endocarditis or glomerulonephritis and food gravis), allograft rejection, allergies, lyme disease, hepatitis, postcrost endocarditis or glomerulonephritis and food streptococcal endocarditis or glomerulonephritis and food cancer, hepatitis.

Carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, carcinal carcinoma, and condyloma acuminatum. The peptides may also be useful as diagnostic or carcinoma, lill be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the election of epitope based vaccines particularly towards conserved conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.
allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;
glomerulonephritis; food hypersensitivity; malaria.
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Pred. No. 4.2e+02;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 46; 60pp; English.
                                                                                                                                                                                                        99WO-US012066.
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                                                                 Unidentified
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The present introduced from those represented by peptides AAY98812-199339 which epitope selected from those represented by peptides AAY98812-199339 which epitope selected from those represented by peptides AAY98812-199339 which care derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less compared selected determinants and could therefore be used to induce a chelper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used to induce a chronic viral diseases and cancer. Examples of diseases that can be created using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and mysathanian acceptance diseases (rheumatoid arthritis, multiple sclerosis, and mysathanian acceptance) allograft rejection, allergies lyme disease, hepatitis, post-creagensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Cancer, hepatitis D, hepatitis C, AIDS, renal carcinoma, cervical cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, and condyloma acuminatum. The peptides may also be carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic creagents, for example, to determine the susceptibility of an individual condyloma suminantum. The peptides may also be individuals will be at substantial risk of development of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved contrability and malariarial and antibalish and an antibalish and an epitopes should sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.
                                         immune response, chronic viral disease, cancer, autoimmune disease,
rheumatodi arthritis, multiple sclerosis; mysathenia gravis, AIDS;
allograft rejection, allergy, lyme disease, hepatitis; prostate cancer;
glomerulonephritis; food hypersensitivity; malaria.
                        Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 48; 60pp; English.
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50.0%;
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Best Local Similarity
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                                                                                                                                                                                                            WO9961916-A1
                                                                                                                                                             Unidentified
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Search completed: November 14, 2004, 13:44:59 Job time : 112.5 secs

HLA class II binding antigen epitope peptide #494.

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Q79A22
Q79A22,
Q79A22,
05-JUL-2004 (TEMBLrel. 27, Cre
f 05-JUL-2004 (TEMBLrel. 27, La
rr.-2004 (TEMBLrel. 27, La
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Matches 5; Conser
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PubMed=12368865;
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SEQUENCE
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                                                                                       November 14, 2004, 13:17:28; Search time 122.5 Seconds (without alignments) 65.757 Million cell updates/sec
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            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                  lotal number of hits satisfying chosen parameters:
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Q76MM5
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Listing first 45 summaries
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Q9S3K8
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Match Length DB
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Nauture 419:1212-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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9 AA; 1001 MW; 4687A5AB476455B7 CRC64;
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Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Created)
                                  Q9R8F2
Q9R8F2
Q9R8F7
Q9R8F7
Q9R8G1
Q9R8G3
Q9R8G6
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EMBL; AABL01002263; EAA18865.1; -.
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100.0%; Pre
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01-MAR-2004 (TrEMBLrel. 26, Las
Hypothetical protein (Fragment)
Name=PY06620;
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Last sequence update) Last annotation update)

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STRAIN=A, Miya M., Tsukamoto K., Nishida M.; Inoud U.G., Miya M., Tsukamoto K., Nishida M.; Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels."; Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stepanov V.M.; "Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Barasporal crystal protein, wax moth-specific (Fragment).
Bacillus thuringlensis.
Bacteris Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Pred. No: 1.1e+03;
0; Mismatches 3; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene synthase 2 (Fragment).
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FEBS Lett. 232:249-251(1988).
PIR; S00616; S00616.
NOW TER 1 1 1
NON TER 11 21
SEQUENCE 11 AA; 1237 MW; C6
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07M154;
01-MAR-2004 (TEMBLYEl. 26, CX
01-MAR-2004 (TEMBLYEl. 26, L6
01-MAR-2004 (TEMBLYEl. 26, L6
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Best Local Similarity 62.5%;
Matches 5; Conservative (
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Best Local Similarity 80.0°
Local 4; Conservative
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     Mitochondrion
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Q7XB05;
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Q7M154
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"Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
                   Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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Actinopterygii, Neopterygii, Teleostei, Anguilliformes,
Eurypharyngidae, Eurypharynx.
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Pred. No. 1.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                        Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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10 AA; 1261 MW; 357BFE29C682DB47 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
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SEQUENCE FROM N.A.
MEDLINE=22967687; PubMed=12949142;
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                                                                                                                                                                                                                                                                                                                                   36.1%;
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Best Local Similarity 40.000
4, Conservative
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SEQUENCE FROM N.A.
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                                                                                                    [1] -
SEQUENCE FROM N.A.
STRAIN=212;
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Name=moxR;
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BAB87140;
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RESULT 3 Q76MM5

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Nishimura M., Matsuo H., Sugiyama M.;
"Blasticidin S-producing Streptomyces morookaensis possesses an enzyme activity with hydrolyzes puromycin.";
FEMS Microbiol. Lett. 132.95-100(1995).
-!- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF THE AMIDE LINKAGE BETWEEN 1TS AMINONUCLEOSIDE AND O-METHYL-L-TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL TEMPERATURE IS 45 DEGREES CELSIUS.
                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
-!- ENZYME REGULATION: STIMULATED BY DIT. STRONGLY INHIBITED BY ZINC
ION, PERROUS ION, CUPRIC ION, MERCHRY ION, N-BROMOSUCCINIMIDE AND
N-ETHYLMALEIMIDE. PARTIALLY INHIBITED BY COBALT ION.
                                                                                                                  Nishimura M., Matsuo H., Nakamura A., Sugiyama M.; Matsuo A. "Purification and characterization of a puromycin-hydrolyzing enzyme from blasticidin S-producing Streptomyces morookaensis."; J. Biochem. 123:247-252(1998).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
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Pred. No. 1.5e+03;
1; Mismatches 3; Indels
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SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;
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-i- MISCELLANEGUS: HAS AN ISOELECTRIC POINT OF 6.4.
60, GO:0004177; F:aminopeptidase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
Aminopeptidase; Hydrolase.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1970;
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                                                                                 STRAIN=JCM4673 / KCC:S-0673;
PubMed=9538199;
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Best Local Similarity 55.6
Matches 5; Conservative
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les 5, Conservative
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"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
EMBL; AX300592; AAP55331.1; -.
EMBL; AX300599; AAP55338.1; -.
NON TER 13 13
                                                                                                                                               Palaisa K.A., Morgante M., Williams M., Rafalski A.;
"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1795-1806(2003).
EMBL; AY300569; AAP5307.1; -.
NON TER 12 12
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Puromycin-hydrolyzi\ng enzyme (EC 3.-.-.) (Fragment).
Streptomyces morookaensis.
                                                                                                                                                                                                                                                                             12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phytoene synthase 2 (Fragment).
                                                                                                                                                                                                                                                                                                           Score 25; DB 2; I
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AA
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                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                  STRAINEY-14;
MEDLINE=22779048; PubMed=12897253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=W-17, and W-50;
MEDLINE=22779048; PubMed=12897253;
                                                                                                                                                                                                                                                                                                             34.7%;
54.5%;
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54.5%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                              Local Similarity 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNPYSAFQVDI 11
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                                                                                                                                                                                                                                                                                                                                                                                    SNPYSAFOVDI 11
                                                                                                                                                                                                                                                                                                                                                                                                                     1 SDTVSKFPVDI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=4577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=psy2;
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                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                               Query Match
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Q7X761,
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                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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P81801
ID P8180
AC P818
AC P818
DT 01-J
DT 01-J
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Inoue J.G., Miya M., Tsukamoto K., Nishida M.; "Evolution of the deep-sea gulper eel mitochondrial genomes: largescale gene rearrangements originated within the eels."; Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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                                                                                                                                                                                                                                                                                                     Iannelli F., Pearce B.J., Pozzi G.;
"The type 2 capsule locus of Streptococcus pneumoniae.";
J. Bacteriol. 181:2652-2654(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 2; Length 12;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=D39;
Pearce B.J., Iannelli F., Pozzi G.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026471; AAD10169.1; -.
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Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AB046485; BAB87156.1; -.
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10 AA; 1293 MW; 356FAE29C682DB47 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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MEDLINE=22967687; PubMed=12949142;
                                                                                                                                                                                                                                                                      MEDLINE=99214122; PubMed=10198036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 44.4
Matches 4; Conservative
                                                                 Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                      NCBI_TaxID=1313;
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      (Fragment).
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SEQUENCE
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Q76MK9
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=A/Hong Kong/503/97;
STRAIN=A/Hong Kong/503/97;
Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
Zhou N.W., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
Subbarao K.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y., Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Inclear export protein NS2 (Fragment).
Influenca A virus (A/Hong Kong/503/97(HSN1)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; HSNI subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nuclear export protein NS2 (Fragment).
Influenca A virus (A/Hong Kong/491/97(HSN1)).
Viruses; SRRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A; HSN1 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 24; DB 2; Length 8; 62.5%; Pred. No. 1.8e+06; Live 1; Mismatches 2; Indels
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF256191; AAK49124.1; -.
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Last annotation update)
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62.5%;
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Q9S550;
01-MAY-2000 (TEMBLrel. 13,
01-MAY-2000 (TEMBLrel. 13,
01-MAY-2000 (TEMBLrel. 13,
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STRAIN=A/Hong Kong/491/97;
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                                                           PRELIMINARY;
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Best Local (
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Q91U21;
                                                        Q91U19
Q91U19;
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098550
ID 09855
AC 09855
DT 01-MA
DT 01-MA
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091021
AC 09102
AC 09102
DT 01-DE
DT 0
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RESULT 10
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"Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";
Mol. Biol. Evol. 20:1917-1924 (2003).
                                                                                                     Silene pentelica.
Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Caryophyllales, Caryophyllaceae, Silene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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MEDLINE=21419634; PubMed=11527472;
Pinferring the Mistory of the polyploid Silene aegaea (Caryophyllaceae) using plastid and homocologous nuclear DNA sequences. Evol. 20:474-481(2001).
EMBL; AJ296133; CAC13025.1; -.
NON_TER 1 1 1
NON_TER 10 10
SEQÜENCE 10 AA; 1108 MW; CFIAB6DIBZCABIA9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                       31.9%; Score 23; DB 2; Length 10; 60.0%; Pred. No. 2.5e+03; ative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB046481; BAB87148.1; -.
Mitchondrion.

NON_TER 10 10
SEQÜENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;
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BAB87148;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burypharynx pelecanoides (pelican eel).
Mitochondrion.
                             Created)
 PRT;
                            01-MAR-2001 (TrEMBLrel. 16, C. 01-MAR-2001 (TrEMBLrel. 16, L. 01-MAR-2001 (TrEMBLrel. 16, L. RNA polymerase II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.9
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=B;
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DVTVD 9
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Q9FS93
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Matches
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Oy 2 NPYSAF 7
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|Db 2 NPYWMF 7
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Search completed: November 14, 2004, 13:41:10 Job time : 122.5 secs

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November 14, 2004, 12:03:21; Search time 33.0638 Seconds (without alignments) 149.815 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_MW PUBL.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_MW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NW PUB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                1 SNPYSAFQVDITID 14
                                                                                                                                                                                                                                                                                                                                           US-09-831-253F-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 23
                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 173, App	Sequence 305, App	Sequence 802, App	Sequence 264, App	Sequence 332, App	Sequence 25, Appl	Sequence 43921, A	Sequence 3097, Ap	Sequence 3097, Ap	Sequence 30, Appl	Sequence 125, App	Sequence 91, Appl
SUMMARIES	US-09-071-838-173	US-09-988-493-305	US-10-014-340-802	US-10-700-330-264	US-10-285-394-332	US-10-162-538-25	US-09-864-761-43921	US-09-880-748-3097	US-10-293-418-3097	US-09-842-776A-30	US-10-230-880-125	US-10-211-462-91
DB	9 5	101	14	17	14	14	σ	10	14	11	14	15
% Query Match Length DB	17	15	15	15	15	20	22	10	10	13	19	23
\$ Query Match	51.4	44.4	44.4	44.4	40.3	40.3	40.3	38.9	38.9	38.9	38.9	38.9
Score	37	32	32	32	29	29	29	28	28	28	28	28
Result No.	1	יח ו	4	ß	9	7	80	6	10	11	12	13

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,838
FLING DATE: 01-MAY-1998
CLASSIFICATION: 800

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:

39, Ap	٠,	736, Ap	5, App	- 4	2, App	151, App 714. App	, Appl	Appli	118, APP 220. App	7, App	7, App	o, App	70, Appl	11, Ap	493, A	, App1	, Appl	28. AD	; O				•																			
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9-88 0-29	-10-286	200	4	10-424	10-481	10-350	10-151	- 6-927	10-334	09-983	09-984	10-41	09-171	10-106	10-029	-10-400	100-00-	09-572		996	10-03	10-13	10-62	<u>,</u>	ALIGNMENTS		3.8	2							B. Acida Thet	Development			♥ .			
SN US	as	an	-Sn 9				4	-	4 4	. 0	0 -	- 4	. 0			-20	בי בי	40	6 US-10	د	3 US	4 US-	7 115	} ~	Æ		812000	atent No. US20020152501A1		t L	,	2 5	nda	1	rt B.	۾ ر			Townsend			
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37.	37.	37.	37.	37.	2	37.	9	9	36.	9	9	9 6	o o	36.	9	4 4	* <	4.4	4	34.	34.		34.			-173	ביים	520020	ORMATI						‡	INVENT	F SEQUENCES:	DENCE	EE: T Two	San Fr	Calif	. US
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14 15	16	18	19	21	22	23	25	56	28	53	30	3 T	33	34	35	9 6	7 0	0 0	40	41		4. 4 G 4				RESULT 1	T/O-60-	Patent	GENER	APPI	APPI	APPI	APPI	APPI	APPLI	TITLE	NUMBER	CORI	¥ 6	រ ប៊	ຮ	ฮ <b>โ</b>
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APPLICANT: FBGGBT, NOBERT D.
APPLICANT: Vadegari, Ramin
APPLICANT: Yadegari, Ramin
APPLICANT: Wadegari, Ramin
APPLICANT: Margosian, Linda
APPLICANT: Margosian, Linda
APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: WUMBER: US/09/177, 206
PRIOR APPLICATION NUMBER: US/09/177, 206
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 173
FEMCENT: TENERAL 175
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Publication No. US20030064419A1
GENERAL INFORMATION:
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Page, Martin John
APPLICANT: Page, Martin John
APPLICANT: Page, Martin John
APPLICANT: Page, Martin John
TITLE OF INVENTION: Proteins, Genes, and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
FILE REFERENCE: 2543-1-024
FILE REFERENCE: 2543-1-024
CURRENT APPLICATION WHORER: US/09/988,493
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Pred. No. 9.1;
2; Mismatches
                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                 Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 173, Application US/10213512
Publication No. US20030110536A1
GENERAL INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                    51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%;
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                                                                                                                                                                                                                                                                                                                                                  1 SNPYSAFQVDITID 14
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Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                        Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRGANISM: Arabidopsis sp. US-10-213-512-173
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XGY: linear
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US-09-988-493-305
                                                                                                                                                                                                   US-09-071-838-173
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APPLICANT: Herath, et al TILE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease FILE REPERINCE: 9195-078
CURRENT APPLICATION NUMBER: US/10/014,340
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.0
SEQ ID NO 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US2004020302A1

Publication No. US2004020302A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Herath, Mudiyanselage Athula Chandrasiri Herath
APPLICANT: Herath, Mudiyanselage Athula Chandrasiri Herath
APPLICANT: Herath, Mudiyanselage Athula Chandrasiri Herath
TITLE OF INNENTION: Proteins and Genes For Diagnosis And Treatment of ErbB2-Related
TITLE OF INNENTION WINBER: US/10/700,330
CURRENT APPLICATION NUMBER: US/2003-11-03
FRIOR FILING DATE: 2003-11-03
FRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PatentIn version 3.1
SEQ ID NO 264
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Pred. No. 64;
2; Mismatches 2; Indels
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Pred. No. 64;
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PRIOR APPLICATION NUMBER: PCT/GB01/01219
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0006695.1
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 308
SEQ ID NO 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 802, Application US/10014340; Publication No. US20030064411A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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SGFQIEETID 14
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US-10-014-340-802
                                                                                                                                                                                                                                    TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-014-340-802
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Sequence 43921
Sequence 63921
Sequen
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REPERBNCE/DOCKET NUMBER: 00786/311001
REPERBNCE/DOCKET NUMBER: 00786/311001
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELEPHONE: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPER: amino acid
STRANDEDESS: NO: US20030113749A1 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 14;
Pred. No. 3.2e+02;
1; Mismatches 2.
APPLICATION NUMBER: US/08/630,052
                    FILING DATE: «Unknown»
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.3
Best Local Similarity 62.5
Matches 5; Conservative
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Xu, Chanting Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTER READABLE FORM:

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

OPERATING SYSTEM: PC-DOS/NS-DOS

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 04-Jun-2002

CLASSIFICATION: <Unknown>
                       DB 17; Length 15;
                                                                                                                                                                                                                                                                                                                              Sequence 332, Application US/10285394
Publication No. US20030228583A1
GENERAL INFORMATION:
APPLICANT: AMACHEN
APPLICANT: FASULO, LISA M.
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
APPLICANT: HOLT, GORDON DUANE
APPLICANT: HOLT, THOMAS R.
TITLE OF INVENTION: BIOWARKERS OF LIVER RESPONSE
FILE REFERENCE: POA-003.01
                                                                             Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 14;
Pred. No. 2.3e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/285,394
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,964
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 412
SOFTWARE: Patentin Ver: 2.1
                       Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTIONS
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Publication No US20030113749A1
GENERAL INFORMATION:
APPLICANT: Brent, Roger
MCCOY, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                       44.48;
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54.5%;
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CORRESPONDENCE ADDRESS:
                 Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                     5 SAFOVDITID 14
                                                                                                                                                                      | ||:: |||
SGFQIEETID 14
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; ORGANISM: Homo sapiens
US-10-285-394-332
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Best Local Similarity
Matches 6; Conserv
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US-10-162-538-25
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à g PRIOR APPLICATION DATA

Gaps

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Sequence 3097, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
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Best Local Similarity 50.0
Matches 4; Conservative
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SEQ ID NO 3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-10-293-418-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SPYDAFDI 10
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Matches 5; Conserv
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US-09-842-776A-30
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-06-15

PRIOR PLILING DATE: 2001-03-16

PRIOR PLILING DATE: 2001-03-16

PRIOR PPLICATION NUMBER: 60/276,248

PRIOR PLILING DATE: 2001-03-16

PRIOR PPLING DATE: 2001-03-16

PRIOR PLILING DATE: 2001-03-21

PRIOR PPLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2,0

LENGTH: 10
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Pred. No. 2.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO ACO06227.1
OTHER INFORMATION: EXPRESSED IN BONDE MARROW, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
US-09-864-761-43921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.3%; Score 29; DB 9; Length 22; Best Local Similarity 54.5%; Pred. No. 3.5e+02; Matches 6; Conservative 1; Mismatches 4; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine Vere: 1.1
SEQ ID NO 43921
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Similarity 50.0%;
4; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 STPSSAFSVSL 11
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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3 SPYDAFDI 10
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Best Local Similarity
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RESULT 10 US-10-293-418-3097

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Sequence 30, Application US/09842776A
| Publication No. US20040023316A1
| Publication No. US20040023316A1
| GENERAL INFORMATION:
| APPLICANT: CONNEX GMBH
| TITLE OF INVENTION: IN THE STOOL
| FILE REFERENCE: 1202-08-15
| CURRENT APPLICATION NUMBER: PCT/EP99/08212
| PRIOR PRIOR PLING DATE: 1999-10-29
| NUMBER OF SEQ ID NOS: 64
| SEQ ID NO 30
| LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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parental information:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PES23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT PILING DATE: 2002-11-27
PRIOR PLING DATE: 2001-11-16
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-12-19
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PLING DATE: 2001-03-11
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2000-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.9%; Score 28; DB 14; Length 10; 50.0%; Pred. No. 2.2e+02;
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ORGANIDSM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNPYS 10
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Sequence 125, Application US/10230880 Publication No. US20030190705A1 GENERAL INFORMATION:

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Sequence 2839,
Sequence 2839,
Sequence 2839,
Sequence 2839,
Sequence 2839,
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Sequence 2839,
Sequence 2839,
Sequence 2839,
Sequence 2839,
Sequence 2839,
Sequence 2839,
Sequence 283,
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Sequence 2839, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVESTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT FILING DATE: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PLICATION NUMBER: 60/276,248

PRIOR PLICATION NUMBER: 60/276,248

PRIOR PLICATION NUMBER: 60/277,379

PRIOR PLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-16

PRIOR PRILING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VET. 2.0
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Pred. No. 3.7e+02;
1; Mismatches 2; Indels
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Best Local Similarity 57.1
Matches 4; Conservative
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SEQ ID NO 2839
3 SIPYTVFQTN 12
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ORGANISM: Homo sapiens
US-09-880-748-2839
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; ORGANISM: Homo sapiens
US-10-293-418-2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PYDAFDI 11
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APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Naturasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-23
PRIOR PELLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR APPLICATION NUMBER: US 60/314,244
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PatentIN Ver. 2.1
LENGTH: 23
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                                                                                                                                                                                                                                                        APPLICANT: WONG, JEFFREY L.
APPLICANT: WONG, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
TILLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 17586/58066
CURRENT APPLICATION NUMBER: 09/990,586
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-10-29
PRIOR PILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-16
SOFTWARE: PALENTING DATE: 2001-16
SOFTWARE: PALENTIN NUMBER: 09/293,854
PRIOR FILING DATE: 2001-16
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 125
LENGTH: 19
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US-10-211-462-91
; Sequence 91, Application US/10211462
; Publication No. US20040033495A1
; PENERAL INFORMATION:
; APPLICANT: Murray, Richard

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Best Local Similarity 42.9 Matches 6; Conservative

ORGANISM: Homo sapiens

US-10-230-880-125 Query Match : ORGANISM: Homo sapiens US-10-211-462-91

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Query Match 37.5%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Search completed: November 14, 2004, 12:26:59 Job time : 33.0638 secs

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November 14, 2004, 11:57:25; Search time 40:5106 Seconds (without alignments) 123.973 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100% Listing first 45 summaries

Post-processing: Minimum Match 08

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Database

genescap1980s:\* genescap1990s:\* genescap2001s:\* genescap2001s:\* genescap2002s:\* genescap2003bs:\* genescap2003bs:\*

Description		Aay92951 Transform	Aay93099 Transform	Aay92948 Transform	-	Aay93059 Transform	_	Aau68498 Human Bre	Abp99093 ErbB2 cel	Ada24180 Alzheimer	Aar42489 Canine ho	Aar67769 Peptide f	Aay23572 Peptide f		5 Synthet	Adl70819 PTP1B pho	PTP1B	PTP1B	PTP1B	Adl70908 PTP1B pho	Add26370 Staphyloc	Aaw42169 T-cell ep	Abr75594 Liver res	Adn07473 Liver res	Adk90209 Human 191	Aaw32131 Interacti
SUMMARIES		AAY92951	AAY93099	AAY92948	AAY93066	AAY93059	AAY93067	AAU68498	ABP99093	ADA24180	AAR42489	AAR67769	AAY23572	AAR34228	AAY17925	ADL70819	ADL70905	ADL70907	ADL70906	ADL70908	ADD26370	AAW42169	ABR75594	ADN07473	ADK90209	AAW32131
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AAB50335 AAM32954 AAM72723 AAM60111		ABP71452 ABR63206 ABP96132 ARR43783	ABP47086 ADG97913 AAB10012 AAB86092	AAB86060 AAY93058 AAR31182 ABG68025 AAW42229
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## ALIGNMENTS

Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis. Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors. Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Transforming growth factor inhibitory peptide #7. (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA. AAY92951 standard; peptide; 14 AA Claim 8; Page 82; 86pp; Spanish. 98ES-00002465. 99WO-ES000375. (first entry) WPI; 2000-411935/35. Borras Cuesta F; WO200031135-A1 Homo sapiens. 23-NOV-1999; 24-NOV-1998; 08-NOV-2000 02-JUN-2000. AAY92951; RESULT 1 AAY92951 THE STATE OF THE S

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

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Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                                                                                  Transforming growth factor inhibitory peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                          (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
              AAY92948 standard; peptide; 15 AA.
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                                              100.0%; Score 72; DB 3; I 100.0%; Pred. No. 1.2e-06;
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100.0%; Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                    AAY93099 standard; peptide; 14 AA.
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial anino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY22945-Y9131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
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  Borras Cuesta F;
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Pred. No. 2.9e-05;
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                       Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 53; DB 3; Length 15; 100.0%; Pred. No. 0.0054; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming growth factor inhibitory peptide P107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Preq. ....
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                                                                                                                                                                                                                             Disclosure; Page 28; 86pp; Spanish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98ES-00002465.
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WPI; 2000-411935/35.
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The invention relates to diagnosing, determining the stage or severity, or indentifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing the effect of therapy on a subject with cancer, and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, and for cancer, for determining the severity of breast cancer, and monitoring cancer, for determining the severity of breast cancer, and monitoring the effect of therapy administered to a subject. Antibodies raised against the binding domain of a BPI, the cancer inhibits the function cancer and encorporated into a pharmaceutical composition for treating or preventing breast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the fewer side effects that other prior art methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the fewer side effects that other prior art methods are more rapid effect with fewer side effects that other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the invention
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               examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
receptors. Peptides AAY92945-Y93133 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying proteins for clinical screening, diagnosis and prognosis of breast cancer, comprises detecting Breast Cancer-Associated Protein Isoforms (BPIs) using two-dimensional electrophoresis.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Breast cancer-associated protein isoform, BPI-279 peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Breast cancer-associated protein isoform; breast cancer; immunogen; cytostatic; BPI; tryptic digest peptide.
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                                                                                                                                                                                                                                    DB 3; Length 15;
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                                                                                                                                                                                                                                  Score 37; DB 3
Pred. No. 5.8;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU68498 standard; peptide; 15 AA.
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                                                                                                                                                 disease, specifically cirrhosis
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                                                                                                                                                                                                                                  51.4%;
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Best Local Similarity 77.5-
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                                                                                                                                                                                           Sequence 15 AA;
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The present invention describes a method for screening or diagnosing ETBS2—related cancer. The method comprises generating ETBS2 overexpression features (EOPS) from test samples of body fluid from the ubject by electrophoresis, and comparing the EOPS in the test sample with that from normal subjects or with an expression reference feature (ERF) in the test sample. Also described: (1) an antibody capable of immunospecific binding to an ETBS2 overexpression protein isoform (EOPI); (2) pharmaceutical compositions comprising an EOPI, a nucleic acid encoding an EOPI, an amount of the above antibody or its fragment, and a carrier; (3) a kit comprising on or more antibodies and/or EOPIs cited above, other reagents and instructions for use; (4) methods of treating or preventing ETBS2-related cancer; (5) methods of screening for or preventing EEDB2-related cancer; (5) method of screening for or identifying agents that interact with or modulate the expression or activity of, one or more EOPIs, EOPI fragment, EOPI-related polypeptides, or EOPI-fusion proteins; (6) a method for modulating the activity of one or more EOPIs, comprising administering to a subject an agent identified by the method of [5]; and (7) a method for identifying are therapy. The method is useful in screening, diagnosing, preventing or treating EEDB2-related cancer, determining the stage or seventity of EIBB2-related cancer, determining the stage or seventity of EIBB2-related cancer, determining the stage or seventity of EIBB2-related cancer, dentifying a subject at the risk of developing EXBB2-related cancer, dentifying a subject at the risk of developing EXBB2-related cancer.

The concern indentifying a subject at the risk of developing EXBB2-related cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing and treating BrbB2-related cancer, comprises generating BrbB2 Overexpression Features (BOFs) from test samples from a subject by electrophoresis, and comparing the BOFs in the sample with a
                                                                                   Gaps
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                                       Length 15;
                                                                                   2; Indels
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                                         DB 4;
51;
                                                                                 2; Mismatches
                                         Score 32;
Pred. No.
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                                                                                                                                                                                                                                                                           ABP99093 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-2001; 2001GB-00010886.
23-NOV-2001; 2001GB-00028183.
                                         44.4%;
60.0%;
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                                                                                   Conservative
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                                                                                                                            5 SAFQVDITID
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                                       Query Match
Best Local Similarity
Sequence 15 AA;
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ABP99093
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of screening or diagnosing Alzheimer's disease in a subject. The method is useful for screening, diagnosis or prognosis of Alzheimer's disease in a subject for determining the stage of severity of Alzheimer's disease in a subject, for identifying a subject at risk of developing Alzheimer's disease, or for monitoring the effect of therapy administered to a subject having Alzheimer's disease. The method is also useful in treating vascular dementia, Lewy body dementia, schizophrenia, Parkinson's disease, multiple sclerosis or depression. The inventive method identifies sensitive and specific biomarkers for the diagnosis of Alzheimer's disease in living subjects. It provides therapeutic agents for Alzheimer's disease that works quickly, potently, specifically with fewer side effects. The present sequence represents the amino acid sequence of a Alzheimer's disease-
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related cancer, and for drug screening or drug development. The kit is useful in carrying out the above methods. ABP98940 to ABP99206 represent specifically claimed EOPIs from the present invention
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening, diagnosis or prognosis of Alzheimer's disease in subject, involves manyzing test sample of brain tissue from subject, and comparing feature in test sample with that of person(s) free from Alzheimer's disease.
                                                                                                                                                                                                                                                                                                  Alzheimer's disease-associated protein isoform tryptic peptide #789.
                                                                                                                                                                                                                                                                                                                         human; Alzheimer's disease; vascular dementia; Lewy body dementia; schizophrenia; Parkinson's disease; multiple sclerosis; depression; Alzheimer's disease-associated protein isoform; ADPI.
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                                                                             Length 15;
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                                                                            Score 32; DB 6
Pred. No. 51;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rohlff C;
                                                                                                                                                                                                                       ADA24180 standard; peptide; 15 AA.
                                                                         44.4%;
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                                                                                                      6; Conservative
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SGFQIEETID 14
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                                                                                       Local Similarity
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                                                    Sequence 15 AA;
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Length 15;

DB 6;

Score 32; DB Pred. No. 51;

44.48;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                            neutrophil inhibitory factor; NIF; glycoprotein; endoparasite; nematode; parasitic worm; canine hookworm; peritoneal inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic acid, vectors, transformed hosts and antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer; neutrophil inhibitory factor; NIF; inflammation; adhesion; endothelial cells; inflammatory response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide fragment of neutrophil inhibitory factor (NIF).
                                                                                                                                                                                                                                                                                      Canine hookworm NIF tryptic fragment T24.
                                                                                                                                            AAR42489 standard; protein; 17 AA.
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(first entry)
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SAFQVDITID 14
                                    SGFOIEETID 14
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02-JUN-1994
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27-FEB-1995
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us-09-831-253f-7.rag

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The specification describes mutant Neutrophil Inhibitory Factors (NIF8), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Gln residue. NIF8 may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid atthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury contrained may be used as vaccines against parastic caused by the bacterial infection such as sepsis or bacterial meningitis. NIF8 or NIF contrained may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection and collecting of NIF from tissue homogenates, cloned cells etc. NIF8 may be useful for the detection of a mammalian host of seclul for the detection of NIF mimics or suseful for the detection of NIF mimics of the NIF and inhibitors may also be used as antihelminic agents. AAY23572-90 represent peptide fragments of a canine hookworm NIF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
                                                                                                        Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 2; Length 17;
Pred. No. 59;
2; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTLV-I gp46 external envelope glycoprotein fragment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                obtained after proteolytic digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR34228 standard; peptide; 21 AA
                                                                                                                                                      Example 9; Fig 7A; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US008405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
               (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAFQVDIT 12
                                             Foster DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-134125/16.
                                                                            WPI; 1999-403975/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAFELDIT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9306843-A1
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04-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR34228;
                                             Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT: 13
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                                                                                                                                                                                                                                                                                        Neutrophil inhibitory factor peptide(s) - derived from nematodes, useful for therapy of inflammatory responses.
                                                                                                                                                                                                                                                                                                                                                               Neutrophil inhibitory factors can be used in compositions to inhibit neutrophil activity e.g. adhesion to vascular endothelial cells, and which are useful in the therapy of conditions which involve abnormal or undesired inflammatory responses. This is a peptide fragment of a neutrophil inhibitory factor from canine hookworm which was designated 124 and obtained by trypsin digestion of the factor. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 17;
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Best Local Similarity 75.0%; Pred. No. 59; Matches 6; Conservative . 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide fragment of canine hookworm NIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY23572 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                      Example 9; Fig 7; 239pp; English
                                                                                                                                                                                                                             Vlasuk GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-008B1721.
92US-00996972.
93US-00060433.
93US-00151064.
                                                                                                                                   92US-00996972.
93US-00060433.
93US-00151064.
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                                                                                                                                                                                                 (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                             Foster DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SAFQVDIT 12
                                                                                                                                                                                                                                                           WPI; 1994-234706/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ancylostoma caninum
               Ancylostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAFELDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 AA;
                                            WO9414973-A1.
                                                                                                        23-DEC-1993;
                                                                                                                                     24-DEC-1992;
                                                                                                                                                    11-MAY-1993;
10-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
23-DEC-1993;
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                                                                            07-JUL-1994
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Length 22;

DB 2;

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                            ADL70819;
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases
                        Matches
                                                                                                              RESULT 15
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ID ADL7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new synthetic hydrophilic peptides (AAY17922-934) that correspond to at least one of antigen determinants of envelope sugar proteins of HTLV-1 and HTLV-11 identified in the B lymphatic corpuscle. When bonded covalently to a carrier molecule, the peptides can induce the production of an antibody having a high titre to the gp46 and sp53 envelope sugar proteins of HTLV-1 and HTLV-11 in mammals. The carrier molecule is preferably a tetanus toxoid and selected from the group of sequences shown in AAX17935-39. The carrier molecule is preferably bonded to the peptide through at least one spacer molecule (preferably a dipeptide glycine). The peptides form effectively immunological response to factors causing virus HTLV-1 and HTLV-11. The method also provides an effective conjugate having the peptide
                                                                                                                                                                                                                                                                                                                                                                                                               Hydrophilic peptide; antigen determinant; envelope sugar protein; HTLV-1;
HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.
                                    sequence of peptide 4 corresponds to residues 129-149 from the HTLV-I
                                              gp46 external envelope glycoprotein. When covalently linked to a carrier mon. the hydrophilic peptide can induce in a mammal the prodn. of high titres of antibodies to gp46 envelope glycoprotein from HTLV-I or -II. The peptide and carrier may be used in vaccines against HTLV-I or -II infection. The peptide may be used in a diagnostic assay to detect the presence and titre of anti-HTLV antibodies. See also AAR34225-57. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic hydrophilic peptide - comprises 25 unit aminoacid that corresponds to at least one antigen determinant of envelope sugar protein(s) of HTLV-I and HTLV-II.
                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                      Synthetic peptide derived from HTLV envelope sugar protein.
                                                                                                                                                                         Length 21;
                                                                                                                                                                                                Indels
                                                                                                                                                                       44.4%; Score 32; DB 2; 54.5%; Pred. No. 77; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                              AAY17925 standard; peptide; 22 AA.
          Claim 4; Page 11; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lymphotropic virus type i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 1; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88US-00153420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89JP-00029551
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                        1 SNPYSAFQVDI 11
                                                                                                                                                                                                                                                SSPYWKFOHDV 11
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                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                               30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP02209889-A
                                                                                                                                              Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                     AAY17925;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic, Antidiabetic, Anorectic, Antiinflammatory, Antimicrobial; Cardiant, Neuroprotective; Protein tyrosine phosphataes inhibitor; phosphopeptide, protein tyrosine phosphatae; cancer; diabetes; obesity; inflammation; multiple sclerosis; anglogenesis-dependent disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to phosphopeptides that inhibit protein tyrosine phosphatase. The phosphopeptides are useful as a medicament or for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intesting ancer), diabetes and/or obsity, inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used for preventing or treating congestive heart failure, neurodegenerative diseases, ischaemic events of the brain or demyalinating diseases. The present sequence is one such phosphopeptide from protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious disease; appetite suppressor; congestive heart failure; neurodegenerative disease; PTPIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hooft Van Huijsduijnen R, Walchli S, Arigoni F;
Score 32; DB 2
Pred. No. 81;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTP1B phosphopeptide, SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein tyrosine phosphatase 1B.
                                                                                                                                                                                                                                                                                                                                                                    ADL70819 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2003; 2003WO-EP050385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 5, Conservative
                                                                        Conservative
                                                                                                                                      1 SNPYSAFOVDI 11
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                                                                                                                                                                             SSPYWKFQHDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
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|:|:|| 6 YNAYQVD 12 Search completed: November 14, 2004, 12:02:14 Job time: 42.5106 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2004, 11:57:25 ; Search time 8.6383 Seconds (without alignments) 155.938 Million cell updates/sec Run on:

US-09-831-253F-7 Title: Perfect score:

1 SNPYSAFQVDITID 14 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

4495 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	calcium-activated	potassium channel	exo-poly-alpha-gal	L-serine dehydrata	duodenase - bovine	formylmethanofuran	exoenzyme C3 - Clo	parasporal crystal	L-2,4-diaminobutyr	glandular kallikre	vespakinin M - hor	hypothetical prote	allatostatin - tob	trypsin (EC 3.4.21	DNA topoisomerase	68K collagen-bindi	hypothetical prote	mast cell proteina	aı	ribosomal protein	unidentified 85K p	glutamate-1-semial	lysophospholipase	Ig heavy chain DJ		enamelin i - bovin	Ig heavy chain CDR	MUC1 enhancer bind	hypothetical prote
SUMMARIES	ID	C39800	PS0446	A48968	816376	869371	A58946	805236	800616	B44854	A54326	A61360	PS0371	A61612	A61334	S43834	A61110	A85659	A35646	A40795	836899	PC2369	A48301	S27351	PH1361	PH1729	S10784	PT0229	59	808209
	DB	5	7	7	N	7	7	~	~	~	~	~	7	~	~	7	~	~	7	~	~	7	N	~	~	N	~	7	~	7
	Query Match Length	22	23	23	16	21	17	22	11	14	13	12	14	15	17	18	19	20	21	11	12	13	16	20	23	23	9	11	14	15
ok	Query Match	43.1	43.1	41.7		37.5	36.1	36.1	34.7	34.7	ä		30.6	ö		。	。	ö	29.9	e.	29.5	ď.	φ.	29.5	٥.	29.5	27.8	27.8	7	27.8
	Score	31	31	30		27	56	56			23	22	22		22	22	22	N	21.5	21	21	21	21	21	21	21	20	20	20	20
	Result No.	7	8	e	4	S	9	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

methane monooxygen	arsenite oxidase I	MHC class II histo	sormatin - sorghum	pregnancy-specific	ribosomal protein	R-phycoerythrin ga	proteochondoitin c	very late antigen-	interphotoreceptor	T cell receptor al	brain-associated s	translation elonga	interphotoreceptor	ermG leader peptid	creatine kinase (E
A48179	A45138	179432	B33174	A44524	836898	G22565	PT0077	A28018	G24417	PH1802	A61392	S59490	D24417	B26930	A53875
N	N	0	~	7	~	~	7	~	~	~	~	~	~	~	~
	8	20	22	23	σ	13	14	14	15	11	18	18	19	19	20
17	_														
27.8 17	27.8	27.8	27.8	27.8	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.4
20 27.8 17	20 27.8	20 27.8	20 27.8	20 27.8	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4	19 26.4

## ALIGNMENTS

RESULT 1 C39800 calcium-activated potassium channel, alternate exon B - fruit fly (Drosophil C;Species: Drosophila melanogaster C;Species: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004 C;Accession: C39800	rosophi] ul-2004
R; Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.	
Science 253, 551-555, 1991	

- fruit fly (Drosophila melanogas

Science 253, 551-555, 1991
A;Tille: A component of calcium-activated potassium channels encoded by the Drosophila A;Tille: A component of calcium-activated potassium channels encoded by the Drosophila A;Reference number: A39800; MUID:91313401; PMID:1857984
A;Accession: C39800
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A Molecule type: mRNA A, Residues: 1-22 <ATK> A, Cross-references: UNIPROT:Q03720 C, Genetics: A, Gene: FlyBase:slo A, Cross-references: FlyBase:FBgn0003429

Gaps .. 0 Query Match
43.1%; Score 31; DB 2; Length 22;
Best Local Similarity 44.4%; Pred. No. 35;
Matches 4; Conservative 4; Mismatches 1; Indels

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RESULT 2

potassium channel protein Slo II - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Adrosophila melanogaster
C;Adrosophila melanogaster
C;Adrosophila melanogaster
C;Adrosophila melanogaster
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bon. Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A;Reference number: JH0697; MUID:92360298; PMID:1497890
A;Accession: PS0446
A;Status: nucleic acid sequence not shown

A; Molecule type: mRNA A; Residues: 1-23 <ADEs. A; Crossidues: 1-23 <ADEs. C; Comment: This potassium channel is activated by calcium. C; Genetics: A; Gene: FlyBase: 810 A; Cross-references: FlyBase: FBgn0003429 C; Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

ö 0; Gaps Query Match
43.1%; Score 31; DB 2; Length 23;
Best Local Similarity 44.4%; Pred. No. 37;
Matches 4; Conservative 4; Mismatches 1; Indels

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parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria: AlAlternate names: delta-endotoxii; parasporal crystal protein positive chain C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: jl-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
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45.5%;
                     37.5%;
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Local Similarity 41.7%;
nes 5; Conservative 5
Query Match
Best Local Similarity 71.4%,
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A; Molecule type: protein
A; Residues: 1-22 <TOR>
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A, Molecule type: protein
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Best Local Similarity
Matches 5; Conserv
                                                                                          1 SNPYSAF
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                                                                                                                                       C;Species: Peptostreptococcus asaccharolyticus
C;Date: 19-Mar-1997 #sequence_revision.19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S16376
R;Grabowski, R.; Buckel, W.
Eur. J. Biochem. 199, 89-94, 1991
A;Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat
A;Reference number: S16224; MUID:91293139; PMID:2065681
A;Accession: S16376
A;Status: preliminary
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C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Datession: S63371
R;Zamolodchikova, T.S.; Vorotyntseva, T.I.; Antonov, V.K.
Eur. J. Blochem: 227, 866-872, 1995
A;Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal A;Reference number: S69371; MUID:95172075; PMID:7867648
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83.3%; Pred. No. 1.3e+02;
iive 1; Mismatches 0;
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A.Residues: 1-21 <2AM>
A.Cross-references: UNIPROT:Q9GLN2
C.Superfamily: trypsin; trypsin homology
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A,Residues: 1-16 <EUR>
A,Cross-references: UNIPROT: P33074
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Best Local Similarity 83.3
Matches 5; Conservative
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7 ANPYAGYQL 15
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Matches 5; Conserv
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formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium to Nalternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentificat C; Species Methanobacterium thermoautotrophicum c; Species Methanobacterium thermoautotrophicum c; Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 04-Feb-2000 C; Accession: A58946 F; Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R. Bur. J. Blochem. 234, 910-920, 1995 A; Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoautot A; Reference number: S63519; MUID:96163477; PMID:8575452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the authors identify this peptide as the amino terminus of chain B, but it apper C;Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdepterin; oxidoreduct?
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Length 21;
   Score 27; DB 2; Pred. No. 1.8e+02;
                                                                               0; Mismatches
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or D and excenzyme excensyme C3 - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Species: Clostridium botulinum
C;Accession: S0236
R;Toratani, S.; Yokosawa, N.; Yokosawa, H.; Ishii, S.I.; Oguma, K.
FEBS Lett. 252, 83-87, 1989
A;File: Immuno-crossreactivity between botulinum neurotoxin type C1 or D ar

ö Gapв ö Length 22; Score 26; DB 2; Length 22; Pred. No. 2.8e+02; 1; Mismatches 5; Indels

R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M. FBBS Lett. 232, 249-251, 1988 A;Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotox A;Reference number: S00615

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Best Local Similarity 66.7
Matches 4; Conservative
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6 FSPFRID 12
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C;Species: Homo sapiens (man)
C;Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Caccession: A54326
R;Riegman, P.H.; Viletstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J. Mol. Cell. Endocrinol. 76, 181-190, 1991
A;Title: Identification and androgen-regulated expression of two major human glandular )
A;Reference number: A54326; MUID:92324494; PMID:1726490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L.2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - Vibrio alginolyticus (fragment)
C.5pecies: Vibrio alginolyticus
C,5pecies: Vibrio alginolyticus
C,5pecies: J1-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C,Accession: B44854; B41817
C,Accession: B44854; B41817
C,Accession: Microbiol. 138, 1461-1465, 1992
A,7tile: Microbiol. 138, 1461-1465, 1992
A,7tile: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from A,Reference number: A44854; MUD:92381494; PMID:1512577
A,Accession: B44854
A,Molecule type: protein
A,Residues: 1-14 < YAM>A,Residues: 1-14 < YAMAA,Residues: 1-14 < 
A;Residues: 1-11 cCHE>
A;Cross-references: UNIPROT:07M154
C;Comment: This toxin is effective against the larvae of Galleria melonella (greater
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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C;Species: Vespa mandarinia
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A61860
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                                                                                                                                                                                                                       Length 11;
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80.0%; Pred. No. 2e+02;
trive 1; Mismatches
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Best Local Similarity 80.0°
Matches 4; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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2 TAFEVDSNI 10
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Best Local Similarity
Matches 4; Conserv
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R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ve A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Retens: preliminary
A;Rolecule type: protein
A;Residues: 1-12 <KIS-
A;Cross-references: UNIPROM:Q7M3T3
C;Superfamily: unassigned animal peptides
C;Keywords: hydroxyproline; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
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C;Species: Manduca sexta (tobacco hornworm)

C;Species: Manduca sexta (tobacco hornworm)

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: A61612

R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991

A;Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.

A;Reference number: A61612; MUID:92052112; PMID:1946359
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A,Residues: 1-15 <KRA>
A,Residues: 1-15 <KRA>
Cross-references: UNIPROT:P42559
C,Keywords: neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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42.9%; Pred. No. 7.7e+02;
tive 3; Mismatches 1;
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C)Accession: A6134

R)Estell, D.A.; Laskowski Jr., M.
Biochemistry 19, 124-131, 1980
Biochemistry 19, 124-131, 1980
A)Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the reacting A)Reference number: A61334; MUID: 80103692; PMID: 7352972
A)Accession: A61334
A)Molecule type: protein
A)Residues: 1-17 - ESTP-
A)Cross-references: UNIPROT: 07M433
C)Comment: This isoform is novel in that it readily dissociates from bovine pancreatic types.
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C.Function:
A.Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds
rejoining; this reaction will lead to the conversion of one topological isomer of DNA to
C.Superfamily: bacterial type I DNA topoisomerase
C.Keywords: DNA binding; DNA replication; isomerase; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CyAccession: 84384

Kylunch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.

Biochem. J. 299, 129-136, 1994

A;Title: Characterization of the CysB protein of Klebsiella aerogenes: direct evidence the A;Reference number: 843834

A)Accession: 843834

A)Accession: 843834

A;Residues preliminary; not compared with conceptual translation

A;Residues: 1-18 < LXN>

A;Residues: 1-18 < LXN>

C;Genetics:

C;Genetics:
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C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-May-1999
trypsin (EC 3.4.21.4) 1 - starfish (Dermasterias imbricata) (fragment)
C;Species: Dermasterias imbricata
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C,Species: Klebsiella sp.
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30.6%; Score 22; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.6%; Score 22; DB 2; Length 17; 66.7%; Pred. No. 1.18+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Superfamily: trypsin; trypsin homology
C, Keywords: hydrolase; protein digestion; serine proteinase
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Best Local Similarity 66.7
Matches 4; Conservative
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Search completed: November 14, 2004, 12:03:13 Job time : 8.6383 secs

4 WSAFFID 10

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Run on:

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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APPLICANT: Obad, Nir
APPLICANT: Obad, Nir
APPLICANT: Siyober, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Wargessian, Linda
APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTON: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086420US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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NEUTROPHIL INHIBITORS
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US-09-927-180-3

US-09-227-357-437

US-08-399-696-89

US-08-44-818-304

US-08-444-818-305

US-08-444-818-305

US-08-447-844A-75

US-08-847-844A-75

US-09-256-609-39

US-09-256-611-39

US-08-256-611-39

US-08-97-597-56

US-08-974-685-15

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(Sequence 63, Application US/08173510B
; Sequence 63, Application US/08173510B
; Patent No. S747296
; GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Sulte 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 173, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
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larity 50.0%;
Conservative ;
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         ORGANISM: Arabidopsis sp
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Best Local Similarity
Matches 7; Conserv
      US-09-177-249-173
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                                                                                                                                                November 14, 2004, 11:57:26 ; Search time 11.0213 Seconds (without alignments) 84.242 Million cell updates/sec
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Sequence 110,
Sequence 110,
Sequence 110,
Sequence 7, Ap
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-173-510B-63
US-08-450-497-63
US-08-650-497-63
US-08-650-497-63
US-08-630-052-23
US-08-630-052-22
US-08-934-222-110
US-08-934-222-110
US-08-934-224-110
US-08-124-23-110
US-08-134-34
US-08-127-499A-18
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                          - protein search, using
                                                                                                                                                                                                                                  US-09-831-253F-7
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 23
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                                                                                                                                                                                                                                           Title:
Perfect score:
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Gaps

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44.4%; Score 32; DB 1; Length 17; 75.0%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOR'D PERfect 5.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
APPLICATION NUMBER: 10-00VEMBER-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/986,972
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 203/226
TELECOMMUNICATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELECX: 67-5510
TELEFAX: (713) 955-0440
TELECX: 67-5510
TELECX: ATTORNEY/SUZANTION: TELECX: ATTORNEY/SUZANTION: TELECX: ATTORNEY/SUZANTION: TELECX: ATTORNEY/SUZANTION: TELECX: ATTORNEY/SUZANTION: TELECX: ATTORNEY/SUZANTION: TELECX: ATTORNEY/SUZANTION: ATTORNEY/SUZANTION: ATTORNEY/SUZANTION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63, Application US/08450497
Patent No. 5919900
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NEUTROPHI
TITLE OF INVENTION: NOVEL NEUTROPHI
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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) MOLECULE TYPE: PEPTIDE
US-08-458-218-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 SAFQVDIT 12
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US-08-450-497-63
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| Patent No. 5789178
| GENERAL INFORMATION:
| TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
| TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
| VORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon
| STREET: Sulte 4700
| STREET: Gaime 4700
| CITY: Los Angeles
| STATE: California COUNTRY: U.S.A.
| ZIP: 90011
| COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
| MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
| MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
| MEDIUM TYPE: SICORGALIS | STATE: COMPUTER IBM COMPATION |
| COMPUTER: IBM COMPATION | SYSTEM: COMPUTER: IBM SYSTEM: COMPUTER: IBM SYSTEM: COMPUTER: SYSTEM: COMPUTER: SYSTEM: SYSTE
                                            COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: storage COMPUTER: EMCOMPACTION COMPUTER: EMCOMPACTION COMPUTER: Word Perfect 5.1

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/173,510B FILING DATE: 2.0 ECC.1993

PRIOR APPLICATION NUMBER: 08/151,064
FILING DATE: 10.NOV.1993

APPLICATION NUMBER: 08/60,433
FILING DATE: 11-MAY-1993

APPLICATION NUMBER: 07/986,972
FILING DATE: 11-MAY-1993

APPLICATION NUMBER: 07/981,721
FILING DATE: 11-MAY-1993

APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992

ATTORNEY-AGENT INFORMATION: NAME: BIGGS, SUZAMNE L.

REGISTRATION NUMBER: 30,158

REGISTRATION NUMBER: 30,158

REGISTRATION NUMBER: 30,158

REGISTRATION NUMBER: 30,158

RELECHONE: (213) 955-0440
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 17 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE
US-08-173-510B-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 SAFQVDIT 12
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TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600

(213) 489-160 (213) 955-0440

TELEFAX:

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44.48;
54.58;
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-116-733-5
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1 SSPYWKFQHDV 11
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                                                                                                                                                                              Score 32; DB 2; Length 17;
Pred. No. 16;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08060433C
; Sequence 13, Application US/08060433C
; Patent No. GTS6211
; GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
STREET: 633 Weet Fifth
CTTY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD FEECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,433C
FILING DATE: 11 May 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/881,721
FILING DATE: 11 May 1992
APPLICATION NUMBER: 07/996,972
APPLICATION NUMBER: 07/996,972
APPLICATION NUMBER: 07/996,972
ATTONNEY, AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                   44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                        6; Conservative
                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: PEPTIDE
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SAFELDIT 8
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Best Local Similarity
Matches 6; Conserv
                                                                                                                    , MOLECULE TYPE:
US-08-450-497-63
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TELEX: 6
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APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jum H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 1; Length 22;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                    SIREET: ILON NORTH GLEBE KOAD
CITY: ARLINGTON
STATE: VIRGINIA
COMPUTER: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MURRER: US/08/116,733
FILING DATE: 07-SEP-1993
CLASSIFICATION NUMBER: 32,955
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
RELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUIROUE CHARACTERISTICS:
US-08-116-733-5

Sequence 5, Application US/08116733

Patent No. 5516632

GENERAL INFORMATION:
APPLICANT: PALKER, Thomas J.
TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
ADDRESSEE: ALONDENCE ADDRESSES:
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Fish & Richardson, P.C. 225 Franklin Street
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US-08-630-052-25
; Sequence 25, Application US/08630052
; Patent No. 6399296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
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US-08-933-402-110
                                                                                                                                                                                                                                     STATE: DC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FILE REFERENCE: 7126-094
CURRENT APPLICATION NUMBER: 05/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56843
LENGTH: 21
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
38.9%; Score 28; DB 4; Les
Best Local Similarity 27.3%; Pred. No. 1.2e+02;
Matches 3; Conservative 5; Mismatches 3;
                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995,
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT'INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAY: 20,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
CTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-270-767-56843
; Sequence 56843, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-934-222-110
; Sequence 110, Application US/08934222
; Patent No. 5928896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-630-052-25
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APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardher
STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 110, Application US/08933402

Patent No. 5948887

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PLOPDY disk
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03-MAY-1996
PRIOR APPLICATION NUMBER: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/051,741
APPLICATION NUMBER: US. 08/051,741
REGISTRATION NUMBER: 33,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%;
57.1%;
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Best Local Similarity 5/...
4, Conservative
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1 NPWTVFQ 7
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USA
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GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                       Score 27; DB 2; Length 14; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: PCT/US94/04294
PRIOR APPLICATION NUMBER: PCT/US94/04294
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,464
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACON, JOHN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 27; DB 2; I
57.1%; Pred. No. 1.1e+02;
tive 2; Mismatches 1;
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REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                  US-08-532-818-110
; Sequence 110, Application US/08532818
; Patent No. 5965698
NO:
....TERISTICS:
.... 14 amino acids
TOPOLOGY: linear
US-09-207-621-110
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Matches 4; Conservative
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NPWTVFQ 7
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NPWTVFQ 7
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US-09-231-797-110
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Sequence 110, Application US/09207621
Sequence 110, Application US/09207621
Sequence 110, Application:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Polypeptides That Include Conformation-
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Mashington
STATE: DC
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
PILING DATE:
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03.4M2-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                       FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 03-MAY-1996
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-MPR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REPERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
      SOFIMARE. CORRELIA APPLICATION DATA:
APPLICATION NUMBER: US/08,
FTI.ING DATE: 19-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.5
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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1 NPWTVFQ 7
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USA
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Patent No. oillus.

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: TINE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction TITLE OF INVENTION: Site of Sequences: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 3; Length 14; Pred. No. 1.1e+02; Mismatches 1; Indels
                       MEDIUM TYPE: F.LOPPY G18K

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 12-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY AGENT INFORMATION:
NAME: ISBGEON, JOHN P.
REFERENCE/DOCKET NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 110:
SEQUIENCE CHARACTERISTICS:
FEMCHALIAN FOR SEQ ID NO: 110:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
RIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
FILING DATE: 03-MAY-1997
FILING DATE: 03-MAY-1997
FILING DATE: 03-MAY-1993
FRICK APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NPYSAFQ 8
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NPWTVFQ 7
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Sequence 110, Application US/08934224

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: D.
Sequence 110, Application US/09231797

Patent No. 6084066

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                       AUNESSEE: Foley & Lardner STREET: Suite 500, 3000 K Street NW CITY: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-APR-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.5
Best Local Similarity 57.1
Matches 4; Conservative
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COMPUTER READABLE FORM:
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GY: linear
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1 NPWTVFQ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-231-797-110
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
3Y: linear
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Best Local Similarity
Matches 4; Conserv
 20007
                                                                                                                                                                                                                                                                               US-08-934-222-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ropology:
Sequence 110, App
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                            ; Search time 27 Seconds (without alignments) 34.387 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-934-222-110
US-08-933-402-110
US-08-933-402-110
US-08-532-818-1110
US-08-934-224-110
US-08-934-224-110
US-08-934-223-110
US-08-934-223-110
US-08-94-22-106-3
US-08-422-106-3
US-08-138-310
US-08-138-33
US-09-177-352-99
US-09-177-439-336
US-09-177-439-336
US-09-177-439-336
US-08-177-439-336
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          478139 segs, 66318000 residues
                                                                              November 14, 2004, 13:32:59
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                                                       - protein search, using sw model
                                                                                                                                            1 SNPYSAFQVDITID 14 **
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
                                                                                                                           US-09-831-253F-7
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                      Copyright
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seq length: 14
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Match
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                                                                                                                                                                        Scoring table:
                                                                                                                                     Perfect score:
                                                       OM protein
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Maximum DB
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                                                                              Run on:
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No.
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Patent No. 5928866

CENERAL INFORMATION:
PAPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Manjumatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
ADDRESSEE: FOLGY & Lardner
STREET: Suite 500, 3000 K Street NW
CITT: Washington
STATE: DC
CONTRY: USA
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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,222

FILING DATE: 19-SEPT-1997

PRIOR APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTONNEY/AGBAT INPORMATION:

NAME: IBACEGON, JOHN P:

REGISTRATION NUMBER: 33,751

S-08-383-474B-75
US-08-464-539B-70
US-08-464-539B-70
US-08-463-076E-114
US-09-400-653A-29
US-09-400-653A-29
US-09-38B-311-20
US-08-366-632-20
US-08-366-632-20
US-08-466-632-20
US-08-466-632-20
US-08-461-77-20
US-09-442-027-20
US-09-442-027-20
US-09-442-027-20
US-08-442-027-20
US-08-442-027-20
US-08-442-027-20
US-08-348-471-20
US-08-442-027-20
US-08-36A-20
US-08-36B-20
US-08-36B-20
US-08-36B-20
US-08-36B-20
US-08-36B-20
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Sequence 110, Application US/08532818
Fatent No. 5965698
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCE: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
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Pred. No. 1.1e+02;
2; Mismatches 1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Isacson, John P. REGISTRATION NUMBER: 33,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 04
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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    Washington
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                                                                                                                                Sequence 110, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINT, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-207-621-110
US-09-207-621-110
NS-09-207-621-110
Sequence III, Application US/09207621
Sequence III, Application US/09207621
SEMERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction S
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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COMPUTER: IBM PC compatible
OMFUTER: IBM PC compatible
OMFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 29-GCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-GCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, JOHN P.
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INPORMATION FOR SEQ ID NO: 110:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 2; I Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner
Suite 500, 3000 K Street NW
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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1 NPWTVFO 7
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NPWTVFO
  NPYSAFQ
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                                                                                            RESULT 2
US-08-933-402-110
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APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%; Score 27; DB 3; 57.1%; Pred. No. 1.1e+02;
    Pred. No. 1.1e+02;
2; Mismatches 1
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APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
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SR: 040433/0148
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STREET: Suite 500, 3000 K Street NW
CITY: Washington
COUNTY: DC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palcel
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                                                                                                                                                                                                            Sequence 110, Application US/08934224
Patent No. 6100044
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04
INFORMATION FOR SEQ ID NO: 110:
    57.1%;
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                          4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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1 NPWTVFQ 7
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US-08-933-843-110
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APPLICANT: EVANS, Herbert J.
TILE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                             Length 14;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                         37.5%; Score 27; DB 2; I 57.1%; Pred. No. 1.1e+02; trive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTINIG DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: U.S. 08/143,364
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
ATTONNEY/AGENT INFORMATION:
NAME: 18ACSON, JOHN P.
REGISTRATION NUMBER: 33,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 33,751
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 ...
                                                                                                                        NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
    APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
                                                                 U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110, Application US/09231797
Patent No. 6084066
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S.
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1.
A; Conservative
                                                                                                                                                                                                                                        14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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1 NPWTVFQ 7
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US-09-231-797-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DC
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Sequence 110, Application US/09413492
Sequence 110, Application US/09413492
Sequence 110, Application US/09413492
Sequence 110, Application US/09413492
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Mashington
STATE: DC
COUNTRY: USA
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APPLICATION NUMBER: US/09/413,492 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 3; I
Pred. No. 1.1e+02;
                         APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA: 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,751
REGISTRATION NUMBER: 33,751
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 33,751
LINGTH: 14 amino acids
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APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
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ER: 040433/0148
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3R: 040433/0148
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FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 57.1
Matches 4; Conservative
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NPYSAFQ 8
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US-08-934-223-110
Sequence 110, Application US/08934223
Patent No. 6147189
Fatent No. 6147180:
Patent No. 6147180:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
APPLICANT: Application Street NW
TITLE OF INVENTION: Site
TITLE OF INVENTION: CONSTRUCTION
TITLE OF INVENTION: Site
TITLE OF INVE
      Constraining Groups Which Flank A Protein-Protein Interaction
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                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT 1997
FILING DATE: 19-SEPT 1997
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
FILING DATE: 03-MAY-1996
FILING DATE: 03-MAY-1996
FILING DATE: 29-OCT-1993
FILING DATE: 29-OCT-1993
ATHORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/934,223
FILING DATE:
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Pred. No. 1.1e+0
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TITLE OF INVENTION: Constraining Group
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLCY & Lardher
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-843-110
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Best Local Similarity
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                                                                                                                                                                                                                                                    COUNTRY:
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INFORMATION FOR SEQ ID NO:
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                                      LENGTH:
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APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
MIDMER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/281,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7;
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                                                                                                  Score 27; DB 3; 1
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 1; 1
Pred. No. 3.8e+05;
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FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
                                                                                                                                                                                                                                              RESULT 10
US-08-281-193-3
; Sequence 3, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
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Patent No. 5589170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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               LENGTH: 14 amino acids TYPE: amino acid
                                                                               Ouery Match
Best Local Similarity 57.1.
مار و 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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1 NPWTVFQ 7
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                                              ; TOPOLOGY:
US-09-413-492-110
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US-08-422-106-3
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Patent No. 5840511

GENERAL INFORMATION:
APPLICANT: Tang, Jim
COMPUTER READABLE FORM:
MEDIUM TYPE: 15
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,716
FILING DATE: 23-OCT-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/281,193
FILING BATE: 27-UUL-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                            1; Indels
                                                                                                                                                      Score 26; DB 1; Length 7;
Pred. No. 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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Pred. No. 3.8e+05;
                                                                                                                                                                                          2; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                      36.1%;
57.1%;
                                                                                                                                                Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
amino acids
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                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
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                TYPE: amino acid
STRANDEDNESS: siz
                                                        linear
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Best Local Similarity
Matches 4; Conserv
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Squence 3, Application US/09927180
| Patent No. 6645736
| GENERAL INFORMATION:
| APPLICANT: Jones, Simon | TITLE OF INVENTION: Calcium Independent Phospholipase A2/B | NUMBER OF SEQUENCES: 25 | CORRESPONDENCE ADDRESS: REQUENCES: 3 | STREET: 87 CambridgePark Drive | CITY: Cambridge | STATE: Massachusetts | CONTRY: US.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: FORM:

MEDIUM TYPE: FLORPY disk

COMPUTER: IBM PC COMPACIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: AUKNOWN>

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/519,223
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                                                                                                                                                                                                          Score 26; DB 3; Length 7; Pred. No. 3.8e+05; 1; Indels
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ATTORNEY/AGBNT INPORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7 amino acids
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STRANDEDNESS: single
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                        4; Conservative
                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
TYPE: amino acid
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                      2 NPYSAFQ 8
                                                                                                                                                                                                                                                                                                                                                                                           1 NPHSGFR 7
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US-09-927-180-3
                                                                                                                                                  US-09-519-223-3
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Sequence 3, Application US/09519223

Patent No. 6274140

GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/55,568B
FILLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: BEOWN, Scott A.
REGISTRATION INFORMATION:
TELEPHONEY(10) 876-5851
FILEPHONEY(10) 1876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8e+05;
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Pred. No. 3.8e+
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brown, Scott A.
REGISTRATION UNBRER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : peptide
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NPYSAFO 8
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1 NPHSGFR 7
   U.S.A.
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CLASSIFICATION:
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HYPOTHETICAL:
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US-09-519-223-3
   COUNTRY:
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Gaps

Sequence 519, App Sequence 70, App1 Sequence 70, App1 Sequence 70, App1 Sequence 70, App1 Sequence 31, App Sequence 15, App Sequence 15, App Sequence 1072, App Sequence 1074, App Sequence 1085, App Sequence 1085, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1108, App Sequence 1112, App Sequence 1112, App Sequence 1113, App Seque

US-09-572-404B-2428 US-10-327-598-519 US-10-039-66-710 US-10-039-645-70 US-10-139-684-70 US-10-139-684-70 US-10-139-684-70 US-10-139-684-70 US-10-625-644-8 US-10-9-855-604-792 US-09-855-604-792 US-09-855-604-792 US-10-85-528-1172 US-10-182-252A-1073 US-10-182-252A-1074 US-10-182-252A-1074 US-10-182-252A-1106 US-10-182-252A-1113 US-10-182-252A-1113 US-10-182-252A-1113 US-10-182-252A-1113 US-10-182-252A-1113 US-10-182-252A-113 US-10-182-252A-113 US-10-182-252A-113 US-10-182-252A-113

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US-09-880-748-3097
Sequence 3097, Ap
Sequence 3097, Ap
Sequence 30, Appl
Sequence 2839, Ap
Sequence 2839, Ap
Sequence 277, Appl
Sequence 27, Appl
Sequence 3, Appli
Sequence 220, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 63, Appl
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                                                                                                                            November 14, 2004, 13:45:09; Search time 94.5 Seconds (without alignments) 52.418 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| CGN2_6/pto
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-293-418-3097
US-09-642-776A-30
US-09-880-748-2839
US-10-293-418-2839
US-10-151-882-26
US-09-927-180-3
US-10-334-726-220
US-10-334-726-220
US-09-995-529-83
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                                                                                                                                                                                                                                                                                                                                                     1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                 1 SNPYSAFQVDITID 14
                                                                                                                                                                                                            US-09-831-253F-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published  
                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                 Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                    Run on:
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2619, Ap 2619, Ap 4377, Ap

Sequence Sequence Sequence

US-09-880-748-2619 US-10-293-418-2619 US-10-149-138-4377

ALIGNMENTS

Sequence 99, Appl Sequence 453, App Sequence 11, Appl

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Sequence 3097, Application US/09880748
; Publication No. US20030059937A1
; GREMEAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-21
; RIOR APPLICATION NUMBER: 60/277,379
; RIOR APPLICATION NUMBER: 60/293,499
; RIOR PRIOR DATE: 2001-03-21
; RIOR APPLICATION NUMBER: 60/293,499
; ROWBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 2.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-09-880-748-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NPYSAFQV 9
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Best Local Similarity
Matches 4; Conserv
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Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-09-880-748-2839
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ORGANISM: Homo sapiens
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                                              SNPYS 10
SNPYS 5
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| Sequence 30, Application US/09842776A
| Publication No. US20040023316A1
| GENERAL INFORMATION:
| APPLICANT: CONNEX GNBH
| TITLE OF INVENTION: IN THE STOOL
| FILE REFERENCE: 41735
| CURRENT APPLICATION NUMBER: US/09/842,776A
| FRIOR FILING DATE: 1999-10-29
| NUMBER OF SEQ ID NOS: 64
| SEQ ID NO 30
| LENGTH: 13
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                                                                                                                                       GENERAL INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICANT: Ruben et al.
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/311,469
PRIOR APPLICATION NUMBER: 60/3140,817
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR PAPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/216,248
PRIOR APPLICATION NUMBER: 60/216,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Complementarity determining region (CDR3) of an OTHER INFORMATION: antibody heavy chain directed to a beta-urease;
OTHER INFORMATION: epitope (alternative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 2.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
38.9%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                    Sequence 3097, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.9%;
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.9
Best Local Similarity 50.0
Matches 4; Conservative
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US-10-293-418-3097
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                                              US-10-293-418-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Gaps
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: G0/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/270,379

PRIOR APPLICATION NUMBER: 60/270,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

NUMBER: OF SEQ ID NOS: 3239

SOFURNARE: PRICH IN VET. 2.00

SEQ ID NOS: 3239
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 27; DB 10; Lt
57.1%; Pred. No. 3.7e+02;
iive 1; Mismatches 2;
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Gaps
           Sequence 3, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.1%; Score 26; DB 9; Length 7; Best Local Similarity 57.1%; Pred. No. 1.4e+06; Matches 4; Conservative 2; Mismatches 1; Indels
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Sequence 118, Application US/10334726
Publication No. US20030211521A1
GENERAL INFORMATION:
APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
TITLE OF INVENTION: BREAST CANCER ANTIGEN
FILLS REFERENCE: 1090-36
CURRENT APPLICATION NUMBER: US/10/334,726
CURRENT FILING DATE: 2003-01-02
FRIOR APPLICATION NUMBER: US/09/645,446
PRIOR APPLICATION NUMBER: PCT/GB99/00866
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-02-0
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATCHING UNCE: 1998-09-20
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATCHING UNCE: 2.0
SEQ ID NO 118
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                              ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYPE: amino acid
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1 NPHSGFR 7
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  US-09-927-180-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based OTHER INFORMATION: ability to selectively bind to endothelial cells
                                                                                                                                                                                                                                                                                Sequence 177, Application US/10286457
Publication No. US20030166004A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JENO GYURIS et al.
TITLE OF INVENTYON: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REFERENCE: GPCI-P01-178
CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SOFTWARE: Patentin version 3.1
SEQ ID NO 177
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APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR FILIAGION NUMBER: 60/293,100
PRIOR FILIAGION NUMBER: 60/293,100
NUMBER OF SEQ ID NOS: 48
SSFTWARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 10
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                                          37.5%; Score 27; DB 14; Length 11; 57.1%; Pred. No. 3.7e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 14; Length 12;
Pred. No. 4.1e+02;
1; Mismatches 0; Indels
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US-10-151-882-26
; Sequence 26, Application US/10151882
; Publication No. US20030059862A1
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                         4; Conservative
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SNPQYDAFDI 10
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ORGANISM: Homo Sapiens
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Best Local Similarity
                                            Query Match
Best Local Similarity
                                                                                                                                    3 PYSAFQV 9
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1 SNPWSA 6
US-10-293-418-2839
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US-10-286-457-177
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RESULT 8

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Query Match
Best Local Similarity
Matches 4; Conserv
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5 SNPYT 9
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APPLICANT: Weich, Nadine S.
APPLICANT: Weich, Nadine S.
APPLICANT: Weich, Nadine S.
APPLICANT: White, David
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Mayers, Rachel E.
APPLICANT: William Salar, Mayers, Rachel E.
APPLICANT: Weish, National Salar, 14610, 32124, 11212 AND 12216, NOVEL SEVEN-TRANSMEMBRANE
TITLE OF INVENTION: PROTEINS/G-PROTEIN COUPLES RECEPTORS
TITLE REPRENCE: Mayers, National Salar, 18/10/400, 991
CURRENT APPLICATION NUMBER: US/10/400, 991
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ORGANISM: Artificial Sequence
FEATURE INFORMATION: Description of Artificial Sequence:predicted
OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:predicted OTHER INFORMATION: peptide
                                                                                                                                                                        36.1%; Score 26; DB 14; Length 9; 66.7%; Pred. No. 1.46+06; 1; Mismatches 1; Indels
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US-10-334-726-220

US-10-334-726-220

Sequence 220, Application US/10334726

PUDLICATION NO. US20030211521A1

GENERAL INFORMATION:

APPLICANT: TAYLOR-PAPADIMITROU, JOYCE

TILE REFERENCE: 1090-36

CURRENT APPLICATION NUMBER: US/10/334,726

CURRENT FILING DATE: 2003-01-02

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 324

SOFTWARE: PATENTING DATE: 1998-09-20

NUMBER OF SEQ ID NOS: 324

LENGTH: 9
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; PUDIICATION No. US20330224417A1
GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Matches 4; Conservative
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3 NPYNLF 8
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4 NPYNLF 9
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US-10-400-991-50
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PRIOR PILING DATE: 2002-07-05
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-08-20
PRIOR PILING DATE: 1999-08-20
PRIOR PLICATION NUMBER: US 10/167,192
PRIOR PLICATION NUMBER: US 09/420,187
PRIOR PLICATION NUMBER: US 09/420,187
PRIOR PLICATION NUMBER: US 09/173,869
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 2003-01-09
PRIOR FILING DATE: 2003-01-09
PRIOR PLICATION NUMBER: US 09/377,429
PRIOR PLICATION NUMBER: US 09/377,429
PRIOR PLICATION NUMBER: US 09/377,429
PRIOR PLING DATE: 1999-08-19
PRIOR PLICATION NUMBER: US 09/11,583
PRIOR FILING DATE: 1999-08-19
PRIOR PLICATION NUMBER: US 09/911,583
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
SPIOR APPLICATION NUMBER: US 09/911,583
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
SPIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 1999-08-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
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US-09-995-529-83

Sequence 83, Application US/09995529

Publication No. US20030099655A1

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Tang, William D.
APPLICANT: Tang, William D.
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P.1X 4976

CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 83

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 14;
Pred. No. 1.4e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Amino Acid Fragment US-10-400-991-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
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RESULT 13

0; Gaps

Length 10;

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Score 25; DB 16;
Pred. No. 7.7e+02;
2; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
                                  PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: Patentin version 3.0
SEQ ID NO 519
                                                                                                                                                                                                                                  h 34.7%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                        ; TYPE: PRT; Canis familiaris; US-10-327-598-519
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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OTHER INFORMATION: sequence located in API2 OR IAP2 OR MIHB at 171-180 and may inter
CTHER INFORMATION: with Sequence 2427 in this patent.
US-09:572-404B-2428
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US-10-327-588-519
Squence 519, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Alyapa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies,
TITLE OF INVENTION: for Making and Using Them
FILE REFERENCE: 01-799-A
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TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 2428
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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        Sequence 83, Application US/0999529;
Publication No. US20040091482A9;
Fublication No. US20040091482A9;
Fublication No. US20040091482A9;
Fubrication No. US20040091482A9;
Fubricant: Huse, Milliam D.
FAPPLICANT: Tang, Ying
TILLE OF INVENTION: Humanized Collagen Antibodies and
TILLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT PILIGNO DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 11;
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: synthetic antibody mutation US-09-995-529-83
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Sequence 2428, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
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80.0%;
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Best Local Similarity 80..
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SEQUENCE FROM N.A.
MEDLINE=20540100; PubMed=11086080;
Vilches C., Gardiner C.M., Parham P.;
"Gene structure and promoter variation of expressed and nonexpressed variants of the KIR2DLS gene.";
J. Immunol. 165:6416-6421(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Killer-cell immunoglobulin-like receptor KIR2DL5.3 (Fragment)
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EMBL, AF064963; AAD09947.1; -.
Hypothetical protein.
NON TER.
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Homo sapiens (Human)
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Best Local Similarity
NCBI_TaxID=9606;
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Q9r5m1 staphylococ
Q8x4g1 escherichia
P82096 litoria rub
P35910 achatina fu
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Q70y57 fuerstia af
P77556 escherichia
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(c) 1993 - 2004 Compugen Ltd.
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Q7xbps plasamodium
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P79940 xenopus lae
Q98tu5 xenopus lae
Aab13374 homo sapien
095553 homo sapien
Q15891 homo sapien
Q7m010 clostridium
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STRAIN=Nine Mile Phase I;
MEDLINE=98348442; PubMed=9683477;
Willems H., Jaeger C., Baljer G.;
"Physical and genetic map of the obligate intracellular bacterium Coxiella burnetii.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
NCBI_TaxID=777;
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8 AA; 993 MW; 046B5AA453772727 CRC64;
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MEDLINE=88118956; Pubmed=2963134;
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Q38366;
01-NOV-1996 (TEMBLEEL 01,
01-NOV-1996 (TEMBLEEL 01,
01-DEC-2001 (TEMBLEEL 19,
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Best Local Similarity 66.70,
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Bacteriophage phi-X174.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DB39911.1 (Novel protein with a Kunitz/Bovine pancreatic trypsin inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide core' domains) (Fragment).
                                                                                                                                                                                                                                                                            Homo sapiene (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,
Geysen J.J.G.H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ488208; CAD32561.1; -.
NON_TER
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                                                                   Query Match 39.6%; Score 19; DB 2; Length 9; Best Local Similarity 57.1%; Pred. No. 1.8e+06; Matches 4; Conservative 2; Mismatches 1; Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Al121778; CAB76644.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                      Receptor.

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SEQUENCE 9 AA, 968 MM; 9DEF85A2D2C69735 CRC64;
EMBL; AF260137; AAG38010.1; -. GO; GO:0004872; F:receptor activity; IEA
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2 SLMVVSM 8
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"A Multifaceted Approach to the Characterization of an Intergeneric
Hybrid Manakin (Pipridae) from Brazil.";
Auk 119:1114-1120(2002).
EMBL, AY136617; AAN16894.1; -.
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Name-beta fibrinogen;
Ilicura militaris (pin-tailed manakin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Ilicura.
                                                                                                                                                                                                                                                                                                                                          Buckley K.J., Hayashi M.;

"Role of premature translational termination in the regulation of
"Role of premature 1714 lysis gene.";
J. Mol. Biol. 198:599-607(1987).
J. Mol. Biol. 298:599-607(1987).
Bubl.; X07809; CAA30668.1;
NON TER
SEQÜENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                   (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 19, Last annotation update)
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NCBI_TaxID=10847;
9 AA.
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Maas S., Kim Y.G., Rich A.; "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two tRNA synthetases.";
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Yan Y., Phan L., Yang F., Talpaz M., Yang Y., Xiong Z., Ng B.,
Timchenko N.A., Wu C.J., Ritz J., Wang H., Yang X.-F.;
"A novel mechanism of alternative promoter and splicing regulates the epitope generation of tumor antigen CMLG6-L.";
J. Immunol. 172:651-660(2004).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1781 TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                           35.4%; Score 17; DB 2; Length 8; larity 66.7%; Pred. No. 1.8e+06; Conservative 1; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor antigen CML66 short isoform (Fragment).
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;
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Homo sapiens (Human).
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                                                                              STRAIN=129/SvJ;
MEDLINE=21231131; PubMed=11331948;
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EMBL; AF521134; AAQ08824.1; -..
                                                                                                                                                    Mamm. Genome 12:387-393(2001).
EMBL; AF328904; AAK19310.1; -.
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NON TER 8 8
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Matches 2; Conserv
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                                                                 SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Antilophia.
NCBI_TaxID=208054;
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Archosauria; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
NCBI_TaxID=196027;
                                                                                                                                                    [1]—
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Marini M.A., Hackett S.J.;
Marini M.A., Hackett S.J.;
Mybrid Manakin (Pipridae) from Brazil.";
Hybrid Manakin (Pipridae) from Brazil.";
EMBL; AY136616; AAN16893.1; -.
NON TER 1 9
SEQÜENCE 9 AA, 992 MW; 8620B37878744AB1 CRC64;
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Marini M.A., Hackett S.J.;
Marini M.A., Hackett S.J.;
Marini M.A., Hackett S.J.;
Marini Manakin (Pipridae) from Brazil.";
Mybrid Manakin (Pipridae) from Brazil.";
Auk 119:1114-1120(2002).
BEMBL; AY136615; AAN16892.1; -.
NON TER
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta fibrinogen (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Adenosine deaminase tRNA-specific 1 (Fragment).
                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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SEQUENCE 9 AA; 992 MW; 8620B37878744AB1 CRC64;
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66.7%; Pred. No. 1.8e+06;
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Name=beta fibrinogen;
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les 2; Conservative
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                                                                                            Chiroxiphia caudata.
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SEQUENCE 9 AA;
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      Mitochondrion.
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Q8X4G1
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Timchenko N.A., Wu C.J., Ritz J., Wang H., Yang X.-F.;
"A Novel Mechanism of Alternative Promoter and Splicing Regulates the Epitope Generation of Tumor Antigen CML66-L.";
Immunol. 172:651-660(2004).
EMBL, AF521134; AAQ08824.1; -.
NON TER 9 9 84, 1128 MW; 555CA37866D73B57 CRC64;
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"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
Cladistics 17:211-226(2001).
EMBL; AF407518; AAL10108.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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MEDLINE=22615572; PubMed=12729892;
Moreno M.U., San Jose G., Orbe J., Paramo J.A., Beloqui O., Diez J.,
Zalba G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Anguimorpha, Varanidae, Va
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Flavocytochrome b-558 alpha polypeptide (Fragment).
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Local Similarity 66.7%; Pred. No. 1.8e+06;
les 2; Conservative 0; Mismatches 1;
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NON TER 8
SEQUENCE 8 AA; 965 MW; FF91
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FEBS Lett. 542:27-31(2003)
                                                                                                                                                                                                Best Local Similarity 66.7
Matches 2; Conservative
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7 WSM 9
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01-JUN-2003
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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SEQUENCE FROM N.A.
MEDLINE=21074933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grobeck E.J., Davis N.W., Lim A., Shanlanta E.T., Potamousis K.A.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
66 kba cell surface adhesin for heparan sulfate (Fragment).
Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TAXID=1280;
                                                                               33.3%; Score 16; DB 2; Length 9; 50.0%; Pred. No. 1.8e+06; tive 1; Mismatches 2; Indels
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Liang O.D., Ascencio F., Fransson L.A., Wadstrom T.;
"Binding of heparan sulfate to Staphylococcus aureus.";
Infect. Immun. 60:899-906(1992).
PIR; A43848; A43848.
NON TER 9 9 9 SEQUENCE 9 AA; 1064 MW; 874CA5A36411A735 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                         3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=z2947
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0; Gaps Query Match 33.3%; Score 16; DB 2; Length 9; Best Local Similarity 50.0%; Pred. No. 1.8e+06; Matches 3; Conservative 1; Mismatches 2; Indels

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Search completed: November 14, 2004, 14:07:05 Job time : 189 secs

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us-09-831-253f-5.closed.rapb

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November 14, 2004, 14:07:12 ; Search time 137 Seconds (without alignments) 23.244 Million cell updates/sec
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// cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
// cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*
// cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*
// cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*
// cgn2_6/ptodata1/pubpaa/USO8_NEW_PUB.pep:*
// cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1568699 segs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:
                                                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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48
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                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 10, Appl	Sequence 7, Appli	Sequence 170, App	Sequence 170, App	Sequence 632, App	Sequence 657, App	Sequence 35, Appl	Sequence 35, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 170, App	Sequence 169, App	Sequence 169, App
SUMMARIES			ID		US-10-231-452-7	US-08-979-847-170	US-10-114-104-170	US-10-182-252A-632	US-10-182-252A-657	US-10-441-626-35	US-10-441-625-35	US-10-441-626-38	US-10-441-625-38	US-10-651-165-170	US-08-979-847-169	US-10-114-104-169
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	æ	Query	Match	54.2	54.2	52.1	52.1	52.1	52.1	20.0	50.0	50.0	50.0	50.0	50.0	50.0
			Score	26	26	25	25	25	25	24	24	24	24	24	24	24
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Gaps

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Query Match 54.2%; Score 26; DB 9; Length 9; Best Local Similarity 66.7%; Pred. No. 1.4e+06; Matches 4; Conservative 1; Mismatches 1; Indels

2 SLMIWT 7

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16	24		σ		-10-182	617,
17	24	50.0	σ	12	US-10-182-252A-631	
18	24		σ	15	US-10-182-252A-656	656,
19	24		σ		US-10-182-252A-658	658,
20	24	50.0	δ	15		685,
21	24	50.0	ტ	15	-10-182	1216,
22	23		-		US-10-052-578-216	216. 7
23	23	7	7	14	-10-05	216.
24	23		_	14	-10-053-498B-2	216
25	23	7	7		US-10-258-146A-74	
26	23	7	7	15	-953-21	219
27	23	47.9	7		US-10-258-144-109	109
28	23	47.9	æ	15	US-10-462-452-475	475,
29	23	7.	8	15	US-10-601-953-604	604,
30	23	47.9	8	16	US-10-322-266-476	476,
31	53	47.9	σ		US-09-845-042-27	27,
32	23	7	6	15	US-10-182-252A-630	630,
33	23	47.9	6	15	US-10-182-252A-655	655,
34	22		9	14	US-10-348-167-40	40,
	22	45.8	æ	œ	US-08-979-847-171	171,
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	22	5	6	6	US-09-751-798-5	Sequence 5, Appli
39	22	S	6	6	-751-798-	ø
	22	'n	σ	6	09-780	1
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45	22		ת	11	US-09-995-529-133	Sequence 133, App
					ALIGNMENTS	
RESILT 1						
US-09-796-744-10	44-10					
; Sequence	10, Ag	Sequence 10, Application US/09796744	an	7097	96744	
; Patent No.	. US2(	US20020098527A1	A1			
GENERAL INFORMATION	NFOKE I		;			
APPLICANT		SHITAKA, KENYA	¥ ,			

APPLICANT: SAKURADA, MIKKIKO
APPLICANT: FURUYA, AKIKO
APPLICANT: FURUYA, AKIKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBATA, KENJI
APPLICANT: YAMASAKI, MOTOO
TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
FILE REFERENCE: 249-170
CURRENT PILING DATE: 2002-01-04
FRICA APPLICATION NUMBER: UP 2000-59508
FRICA APPLICATION NUMBER: UP 2000-69508
FRICA REPLING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PALENTIN Ver. 2.1
SOFTWARE: PALENTIN Ver. 2.1
SOFTWARE: PALENTIN Ver. 2.1
SENGIF: DEPT. TYPE: PRT ORGANISM: Mus musculus US-09-796-744-10

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MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                    ö
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFFWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSIFCATION: JUNKNOWN>

PRIOR APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOW-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REGISTRATION NUMBER: 30,024

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               Score 25; DB 8; Length 8; Pred. No. 1.4e+06; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
WPB 39046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 170, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-836-6400
                                                                                  INFORMATION FOR SEQ ID NO: 170: SEQUENCE CHARACTERISTICS: LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                      52.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 210
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                            ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-979-847-170
                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                              1 TSLMIWIM 8
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Sequence 170, Application US/08979847

Septication No. US2003039664A1

GENERAL INFORMATION:
APPLICANT: BERROW, HERVE
APPLICANT: BEDIN, FREDERIC
APPLICANT: BEDIN, FREDERIC
APPLICANT: COMUNITAN-PRABEL, FLORENCE
APPLICANT: MADIRARD, BERNARD
APPLICANT: MADIRARD, BERNARD
APPLICANT: GARSON, JEREMY
APPLICANT: GARSON, JEREMY
APPLICANT: TUKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
                                                                                                Sequence 7, Application US/10231452
Publication No. US20030175273A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TANAKA, AKIKO
APPLICANT: TOWENTION: HUMAN CDR GRAFTED ANTIBODY ANTIBODY FRAGMENT THEREOF
FILE REPREBRENCE: 249-273
CURRENT APPLICATION NUMBER: US/10/231,452
CURRENT APPLICATION NUMBER: JP 2001-265144
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver: 2.1
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COUNTRY: USA
ZIP: 2320
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vergion #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
TITING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: OLIFF & BERRIDGE, PLC
P.O. BOX 19928
ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SLMIWT 7
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4 SLLFWT 9
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STREET: P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-979-847-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-231-452-7
                                                                                     US-10-231-452-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7
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GENERAL INFORMATION:
APPLICANT: Gualfetti, Peter
APPLICANT: Gualfetti, Peter
APPLICANT: Gualfetti, Peter
APPLICANT: Hitchinson, Colin
APPLICANT: Phillips, Jay lan
TITLE OF INVENTION: No. US20030186418Alel Variant EGIII-Like Cellulase
FILE REFERENCE: GG631
CURRENT APPLICATION NUMBER: US/10/441,626
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide US-10-182-252A-657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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US-10-441-625-35

Sequence 35, Application US/10441625

Publication No. US2003203467A1

GENERAL INFORMATION:
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
TITLE OF INVENITON: Compositions
TITLE OF INVENITON: Compositions
FILE REFERENCE: GG631
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 35
LENGTH: F

TYPE: PRIFE T

ORGANISM: Artificial Sequence

FEATURE:

                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              52.1%; Score 25; DB 15; 28.6%; Pred. No. 1.4e+06; iive 5; Mismatches 0
                    PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SEGTWARE: PatentIn Ver. 2.1
SEQ ID NO 657
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-441-626-35; Sequence 35, Application US/10441626; Publication No. US20030186418A1
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.6
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: BOX2
US-10-441-626-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SLMIWIM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AIVVWTL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQUENCE 632, Application US/10182252A

SQUENCE 632, Application US/10182252A

SQUENCE 632, Application US-102040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGARD, ANDERS

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SANNE LISE

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SYLVIB

APPLICANT: CORBET, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: CONTROL OF HIV INFECTIONS

TITLE OF INVENTION: CONTROL

PRIOR PLICATION NUMBER: US/10/182,252A

CURRENT FILING DATE: 2003-04-10

PRIOR PLING DATE: 2001-01-29

PRIOR PLING DATE: 2000-01-31

NUMBER OF SED ID NOS: 1388

NUMBER OF SED ID NOS: 1388

NUMBER OF SED ID NOS: 1388

LENGTH FOR
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APPLICANT: BUNDAK, SOREN
APPLICANT: BUNDAK, SOREN
APPLICANT: BUNDAK, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUGEMOLIER, SANNE LISE
APPLICANT: LAUGEMOLIER, SANNE LISE
APPLICANT: LAUGEMOLIER, SANNE LISE
APPLICANT: LANSEN, JAN
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT PILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-029
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 2000-01-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                      Score 25; DB 14; Length 8; Pred. No. 1.4e+06; 2; Mismatches 2; Indele
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SEQUENCE DESCRIPTION: SEQ ID NO: 170: US-10-114-104-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6

US-10-182-252A-657

US-10-182-252A-657

Sequence 657, Application US/10182252A

Publication No. US20040072162A1

GENERAL INPORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: FOMSGAARD, ANDERS
                                                                                                                   Query Match 52.1%;
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity 28.0
Local 2; Conservative
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TSQLTWTV 8
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APPLICANT: BESEME, FREDERIC
APPLICANT: COULVET-FREYNAND, COLETTE
APPLICANT: COULVET-FREYNAND, COLETTE
APPLICANT: MANDRAND, BERNARD
APPLICANT: MANDRAND, BERNARD
APPLICANT: MANDRAND, BERNARD
APPLICANT: MANDRAND, SERVIARD
APPLICANT: THIS, PHILIP
APPLICANT: 
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VRUS
TITLE OF INVENTION: VINUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT FILING DATE: 1993-09-02
PRIOR APPLICATION NUMBER: BC/08/974,690C
PRIOR PILING DATE: 1994-10-19
PRIOR PELING DATE: 1994-10-29
PRIOR PELING DATE: 1994-10-20
PRIOR PILING DATE: 1994-10-20
PRIOR PILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATENTIN VARIENCE PATENTIAL DATE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 24; DB 15; Length 7; 66.7%; Pred. No. 1.40+06; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: OLIFF & BERRIDGE, PLC
: P.O. BOX 19928
ALEXANDRIA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Sequence 170, Application US/10651165
Publication No. US20040047877A1
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Publication No. US20030039664A1
GENERAL INFORMATION:
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ORGANISM: hepatitis C virus
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Matches 4; Conserv
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             LMIW
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US-10-41-626-38
US-10-41-626-38
| Sequence 38, Application US/10441626
| Publication No. US20030186418A1
| GENERAL INFORMATION:
| APPLICANT: Gualfetti, Petin
| APPLICANT: Mitchinson, Colin
| APPLICANT: Phillips, Jay Ian
| TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase
| TITLE OF INVENTION: Compositions
| TITLE OF INVENTION: Compositions
| TITLE OF INVENTION: US0030186418A1el Variant EGIII-Like Cellulase
| TITLE OF INVENTION: Compositions
| TITLE OF INVENTION: Good Of US0030186418A1 626
| CURRENT FILING DATE: 2003-05-19
| NUMBER OF SEQ ID NOS: 64
| SEQ ID NO 38
| LENGTH: 6
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                                                                                                                                          Length 5;
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US-10-441-62E-38
Sequence 38, Application US/10441625
Sequence 38, Application US/10441625
Sequence 38, Application US/10441625
Sequence 38, Application No. US2003020467A1
SEPERAL INFORMATION:
APPLICANT: MITCHINSON, Colin
APPLICANT: Phillips, Jay Ian
TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
TITLE OF INVENTION: Novel Variant
FILE REFRENCE: GC631
CURRENT FILING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
SEQ ID NOS: 64
LENGTH: 6
LENGTH: 6
                                                                                                                                50.0%; Score 24; DB 14; I
100.0%; Pred. No. 1.4e+06;
ative 0; Mismatches 0;
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                                                                                                                            Query Match
Best Local Similarity 100.
Matches 4; Conservative
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US-10-441-626-38
; OTHER INFORMATION: BOX2
US-10-441-625-35
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: FUNDARA, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: CONTENCY. CORBET, SYLVIE
APPLICANT: LAURMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT PILING DATE: 2003-04-10
FRIOR APPLICATION NUMBER: PCT/DK01/00059
FRIOR PILING DATE: 2000-01-28
FRIOR PILING DATE: 2000-01-28
FRIOR PILING DATE: 2000-01-31
FRIOR PILING DATE: 2000-01-31
FRIOR APPLICATION NUMBER: US 60/179,333
FRIOR PILING DATE: 2000-01-31
FRIOR PILING DATE: 2000-01-31
FRIOR PILING DATE: 2000-01-31
FRIOR APPLICATION NUMBER: US 60/179,333
FRIOR PILING DATE: 2000-01-31
FRIOR APPLICATION NUMBER: US 60/179,333
FRIOR PILING DATE: 2000-01-31
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APPLICANT: FONGGARD, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: LAUEMOLLER, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: COMPROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
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US-10-182-252A-3
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0
                                                                                                                                                                       Length 8;
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                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                 50.0%; Score 24; DB 14;
57.1%; Pred. No. 1.4e+06;
iive 1; Mismatches 2;
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Pred. No. 1.4e+06;
5; Mismatches 0
                            TOPOLOGY: linear
HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-10-114-104-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/182,252A
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PRIOR APPLICATION NUMBER: PCT/DK01/00059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10182252A Publication No. US20040072162A1 GENERAL INFORMATION: APPLICANT: FOMSGAARD, ANDERS
        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 28.6
Matches 2; Conservative
                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserve
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                                                                                                                                                                       Query Match
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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COMPUTER: IBM PC compatible

CORPUTER: IBM PC compatible

SOSTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSITCATION NUMBER: 08/979,847

RILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REGISTRATION NUMBER: 90.024

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0%; Score 24; DB 8; Length 8; Best Local Similarity 57.1%; Pred. No. 1.4e+06; Matches 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLLFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-114-104-169
; Sequence 169, Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
; APPLICANT: PEREON, HERVE
; APPLICANT: PEREON, HERVE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 169:
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET WUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-640
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-979-847-169
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## PRIOR FILING DATE: 2001-01-29

## PRIOR APPLICATION WINBER: BP 00610017.6

## PRIOR APPLICATION WINBER: BP 0061017.6

## PRIOR PILING DATE: 2000-01-38

## PRIOR PILING DATE: 2000-01-31

## PRIOR PILING DATE: 2000-01-31

## NUMBER OF SEQ ID NOS: 1388

## NUMBER OF SEQ ID NOS: 1388

## SEQ ID NO 215

## LENGTH: 9

## CORPANISM: Artificial Sequence

## FEATURE: PRT

## ORGANISM: Artificial Sequence

## CORPANISM: Artificial Sequence

## FEATURE: PRT

## ORGANISM: Artificial Sequence

## FEATURE: PRT

## FEATURE
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HIV A24 8
HIV B62 8
HIV A24 8
HIV A01 8

Aau87812 Aby3892 Abp18425 Abp22274 Abp1658 Abp16597 Abp16597 Abp14227 Aaj00551 Aaj001178 Aaj01178 
Hepatitis Hepatitis Hepatitis Hepatitis MSRV-1 PO

Scoring table:

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Database

Perfect score:

Sequence:

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor, liver; extracellular matrix degradation inhibitor; mimetope, cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming growth factor inhibitory peptide P142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
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                                                                                     AAU87812
AAY33692
ABP18425
ABP1658
ABP16583
ABP16583
ABP11934
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AAJ01013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93096 standard; peptide; 9 AA.
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                                                                                                                                                   ; Search time 156 Seconds (without alignments) 20.696 Million cell updates/sec
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Compugen Ltd.
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                    version 5
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                                           Copyright
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Score

Result Š.

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This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                               pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 179; 220pp; English.
                                                                                                                Human papillomavirus peptide #514.
                ADK08459 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                              24-JUL-2003; 2003WO-EP008112.
                                                                                                                                                                                                                                                                                                                            24-JUL-2002; 2002AT-00001124.
11-JUL-2003; 2003EP-00450171.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt W.
                                                                                                                                                                                              Human papillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AXY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or
                                                                                                                                                                                                                                                                                                                                                         Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor, liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Borras Cuesta F;
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                                                Length 9;
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                                             Score 48; DB 3; I
Pred. No. 1.7e+06;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, specifically cirrhosis
                                             100.0%;
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Habel A;

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                             Gaps
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Score 28; DB 8; Length 9; Pred. No. 1.7e+06; 5; Mismatches 0; Indels
                                                                                                                                                                                                                              Human papillomavirus peptide #150.
                                                                                                                                                 ADK08095 standard; peptide; 9 AA.
h 58.3%;
Similarity 37.5%;
3; Conservative !
                                                                                                                                                                                                  06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                           Human papillomavirus.
                                                     σ
  Query Match
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ADK08449;
(SCAN/)
(ALEX/)
                                (OLDL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK08449
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                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                  reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antigen; NY-ESO-1; cancer; SEREX; cytostatic; immunosuppressive; serological identification of antigens by recombinant expression cloning; melanoma; hepatoma; lymphoma; breast cancer; prostate cancer; lung cancer; ovarian cancer; thyroid cancer; bladder cancer; infection; autoimmune disorder; cancer marker; CTL; cytolytic T cell line; human leukocyte antigen; HLA binding motif.
                                                                                                                                          New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
                                                                                                                                                                                                        This invention relates to a novel polypeptide encoded by an alternative
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                            Score 28; DB 8; Length 9;
Pred. No. 1.7e+06;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NY-ESO-1 HLA binding motif #21.
                                                                                                                                                                                    Claim 18; Page 175; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU64837 standard; peptide; 9 AA.
                                                                                                     Habel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-1996; 96US-00725182.
15-SEP-1997; 97US-00937263.
29-DEC-2000; 2000US-00751798.
                              24-JUL-2003; 2003WO-EP008112.
                                                 24-JUL-2002; 2002AT-00001124.
                                                                                                                                                                                                                                                                                                                                             58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-2001; 2001US-00023182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
                                                                                                     Mattner F, Schmidt W,
                                                                               (INTE-) INTERCELL AG
                                                                                                                        WPI; 2004-169243/16
                                                                                                                                                                                                                                                                                                                                                                                    2 SLMIWIMM 9
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002164665-A1.
                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2002
         05-FEB-2004
                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU64837;
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The invention relates to an isolated antibody or binding fragment of antibody, which binds with a protein that is encoded by an isolated nucleic acid molecule the complementary sequence of which hybridises undeled acid molecule the comprising the undeled acid molecule comprising the nucleotides 54-593 of the human cancer marker NY-ESO-1 cDNA appearing as uncleotides 54-593 of the human cancer marker NY-ESO-1 cDNA appearing the nucleotides 54-593 of the human cancer marker NY-ESO-1 cDNA appearing the monoclonal antibody, sereening for cancer in a sample (by contacting the sample with the isolated antibody, and determining binding of the novel antibody to a target as an indicator of cancer), determining antibodies antibody to a target. as an indicator of cancerous condition (by monitoring a cancerosisted artigen in a sample, determining antibodies cancerous condition by a supject or a peptide derived from NY-ESO-1 protein, with the amount of the parameter is cantibody that binds to it, where the amount of the parameter is and treating a subject afflicted with a cancerous condition by administering to the subject an antibody that specifically binds to NY-ESO-1 protein or to an ESO-1 derived peptide (e.g. a peptide identified as stimulating a CTL (cytolytic T cell line) identified by SEREX (serological identification of antigens by recombinant expression cloning) expressed on a cancerous condition) where the antibody is coupled to an anticancer agent. The antibody is useful for treating cancer, e.g. melanoma, belader cancer, conditions or breast, prostate, lung, ovarian, thyroid or bladder cancer, infections or autoimmune disorders. The present sequence represents an expense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                  New antibody that binds to the cancer associated antigen NY-ESO-1, useful for treating cancer, e.g. melanoma, hepatoma, lymphoma, or breast, prostate, lung, ovarian, thyroid or bladder cancer, infections or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                 Old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                             Chen Y, Scanlan M, Alexander K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 6; Length 9; Pred. No. 1.7e+06; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 6; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus peptide #504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK08449 standard; peptide; 8 AA.
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66.7%;
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                                                                                                                                                                             Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disorders.
CHEN Y.
SCANLAN M.
ALEXANDER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus.
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Best Local Similarity
                                                                                                                                                                                                                                                WPI; 2003-298695/29.
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4 SLLMWT 9
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                                                                                                       OLD L J.
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                                                                                                                                                                             Stockert E,
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for treating

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Claim 18; Page 174; 220pp; English.
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                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antiganic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present
                                                                                                                                                                                                                            New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
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                                                                                                                                                                                                                                                                                                               Claim 18; Page 178; 220pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus peptide #143.
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11-JUL-2003; 2003EP-00450171.
24-JUL-2003; 2003WO-EP008112
                                       24-JUL-2002; 2002AT-00001124
11-JUL-2003; 2003EP-00450171
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                                                                                                                                                  Mattner F, Schmidt W,
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                                                                                                      (INTE-) INTERCELL AG
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                                                                                                                                                                                         WPI; 2004-169243/16.
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ALVLWTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK08088;
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AZ ADKO
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AZ ADKO
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DT 06-M
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CS Huma
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This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antidenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes a gene recombinant antibody that can specifically react with the extracellular domain of human CCR4. The antibody and its fragment are applicable in diagnosis and development of drugs for Th2-mediated immune diseases and blood cancer including bronchial asthma, atrophic dermatitis and leukemia. The present sequence represents a complementarity determining region (CDR) of the light chain variable region of an antibody directed against human CCR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity determining region 3 of light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene recombinant antibody; CCR4; Th2-mediated immune disease; blood cancer; bronchial asthma; atrophic dermatitis; leukemia
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 8; Length 8;
Pred. No. 1.7e+06;
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Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 101; 116pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG67672 standard; peptide; 9 AA.
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Yamasaki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2001; 2001WO-JP001656.
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28-DEC-2000; 2000JP-00401563.
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42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shitara K, Hana-
''-n R, Shibata K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-565496/63
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ALVLWTL 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2001
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Mattner F, Schmidt W, Habel A;
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                                                                                                                                                 Ueda R,
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel human CDR-grafted antibody, or its fragment. The antibody or fragment reacts specifically with the extracellular region of human CC Chemokine receptor 4 (CCR4) but shows no reactivity toward human platelets. The antibody of the invention has cytostatic, antiallergic, antiinflammatory and immunomodulator activity. The antibodies and their fragments are applicable in the diagnosis and treatment of e.g. cancer and immune diseases. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; diagnosis; interstitial pneumonia; anti-CCR4 antibody;
                                                                                                                                                                  Mouse; CDR-grafted antibody; CC chemokine receptor 4; CCR4; cytostatic; antiallergic; antiinflammatory; immunomodulator; cancer; immune disease.
                                                                                                                                                                                                                                                                                                                                                        Human CDR-grafted antibodies and their fragments specifically reacting with extracellular regions of human CCR4 and cytotoxic to cells expressing it, applicable in diagnosis and drugs for e.g. cancer.
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 1; Indels
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                                                                                                                                                                                                                                                                                                                     Koike
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Pred. No. 1.7e+06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                     Tanaka A,
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse anti-CCR4 antibody light chain CDR3
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 109; 144pp; Japanese
                                                                                                                                                                                                                                                                                                                     Hosaka E,
                                                                                     ABR40267 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                          30-AUG-2002; 2002WO-JP008828.
                                                                                                                                                                                                                                                                              31-AUG-2001; 2001JP-00265144.
                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                               Murine peptide SEQ ID NO: 7.
                                                                                                                            (first entry)
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                     Shitara K, Nakamura K,
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Best Local Similarity
Matches 4; 'Conserv
                   SLMIWT 7
                              ||: ||
SLLFWT
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SLLFWT
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                                                                                                                                                                                                Mus musculus:
                                                                                                                           24-JUN-2003
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                                                                                                        ABR40267;
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Matches
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                                                                  RESULT 9
ABR40267
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prevention of interstitial pheumonia containing anti-CCR4 antibody and/or anti-CCR3 antibody. The reagents are used for the diagnosis, prevention and treatment of interstitial pneumonia. The invention provides a method for distinguishing atypical from typical idiopathic interstitial pneumonia, since the former involves infiltration of mainly Th1 cells malority of the latter involves infiltration of both Th1 and Th2 cells with a majority of the latter. This sequence represents the complementarity determining region 3 (CDR3) from the mouse anti-CCR4 antibody light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to diagnostic reagents and agents for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agents containing anti-CCR4 and/or anti-CXCR3 antibody for diagnosis, prevention and treatment of interstitial pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogenic virus, alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
anti-CXCR3 antibody, Th1 cell infiltration, Th2 cell infiltration, complementarity determining region.
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Pred. No. 1.7e+06;
I; Mismatches 1;
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                                                                                                                                                                                                                                                                       28-FEB-2003; 2003WO-JP002372.
                                                                                                                                                                                                                                                                                                                                     28-FEB-2002; 2002JP-00054764.
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11-JUL-2003; 2003EP-00450171.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004011650-A2.
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pathogenic

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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid aequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of
                                                                                                                                                                                                                                                                                           This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antiganic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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                                                                                                polypeptide encoded by an alternative reading frame of a path
is comprising an antigenic determinant, useful for treating or
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Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing an infection with the pathogenic virus
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                                                                                                                                                                                                                                    Claim 18; Page 179; 220pp; English.
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(first entry)
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Baker DM, Celis E,
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                               WPI; 2004-169243/16.
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15-JUL-2002
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particularly when compared to the use of whole antigens in vaccine antigens. There is evidence that the immune response to whole antigens is directed largely toward variable response to whole antigens is directed largely toward variable response to whole antigen, and myour-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to composition of the groups, carla and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte, CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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group-based vaccines has several advantages over traditional vaccines
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Matches 2; Conservative
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Baker DM, Celis E,
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15-JUL-2002
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ABP19699
ID AXC ABP19
AXC ABP19
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DY 11-SE
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DY 11-SE
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                                            an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of groups that may be present additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. Applisol to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuke PW;
compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSRV; multiple sclerosis; rheumatoid arthritis; gag; pol; reverse transcriptase; ribonuclease H; antigen; immunogen.
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beseme F, Bedin F, Paranhos-Baccala G; adel F, Jolivet-Reynaud C, Mandrand B,
                                                                                                                                                                                                                                                                                               Score 25; DB 4; 1
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Fig 31; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB84465 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSRV-1 POL2B octapeptide #27.
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                                                                                                                                                                                                                                                                                               52.1%;
25.0%;
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KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
MANDRAND B.
GARSON J A.
TUKE P W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00756429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                SLMIWIMM 9
                                                                                                                                                                                                                                                                                                                                                                                   1 AIVVWTIV 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komurian-Pradel F,
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERRON H.
BESEME F.
BEDIN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003039664-A1
                                                                                                                                                                                                                                                              Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB84465;
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(MAND/)
(GARS/)
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(KOMU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERR/)
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milituriar bilitations of the managements of the main included are a process for artificial or defined peptides (including immunodominant peptides). Droteins or defined peptides (including immunodominant peptides, antigenic peptides or conserved motifs). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis, a prime associated with multiple sclerosis or rheumatoid arthritis, a prime associated with multiple sclerosis or rheumatoid a arthritis, a prime for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid a arthritis, a polypeptide exhibiting an inhibitory activity on the proteclytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by and an entibody directed against the MSRV-1 virus obtained by immunogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is an MSRV immunogenic or antigenic peptide (or a conserved peptide motif). Note: The SEQ ID numbers in the sequence listing. Consequence the sequences mentioned in the claims
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid which comprises the pol
gene of a retrovirus associated with multiple sclerosis or rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuke PW;
  multiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid and their fragments having the pol gene of a retrovirus, useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   may not be the sequences the authors intended to claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perron H, Beseme F, Bedin F, Paranhos-Baccala G;
Komurian-Pradel F, Jolivet-Reynaud C, Mandrand B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 170; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG14911 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 AA;
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arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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Sequence 8 AA;

ö Gaps ö Query Match 52.1%; Score 25; DB 8; Length 8; Best Local Similarity 50.0%; Pred. No. 1.7e+06; Matches 4; Conservative 2; Mismatches 2; Indels

1 TSLMIWTM 8 | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : q

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Search completed: November 14, 2004, 14:03:53 Job time: 158 sec8

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MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID
US-08-979-847B-170
 RESULT 1
Sequence 170, App Sequence 35, Appl Sequence 20, Appl Sequence 170, App Sequence 170, App Sequence 170, App Sequence 17, Appl Sequence 17, Appl Sequence 160, App Sequence 160, App Sequence 160, App Sequence 385, App Sequence 171, App Sequence 171, App Sequence 171, App Sequence 135, App Sequence 385, App Sequence 385, App Sequence 171, App Sequence 171
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                                                                                                                  November 14, 2004, 13:58:00 ; Search time 36 Seconds (without alignments) 16.579 Million cell updates/sec
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Sequence 44, P
Sequence 5, Ap
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Aa_COMB.pep:*
/cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-632-570-35
US-08-632-570-38
US-08-632-570-38
US-08-632-570-38
US-08-974-690C-170
US-08-974-685-180
US-08-974-685-180
US-08-974-685-180
US-08-974-685-180
US-09-648-938A-17
US-09-548-938A-17
US-09-58-754-385
US-09-722-550D-385
US-09-722-550D-385
US-09-182-550D-385
US-09-182-550D-385
US-09-183-931-44
US-09-183-931-44
US-09-183-931-6
US-09-182-25-5
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                                                                                                                                                                                                                                                                                                               478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
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Match Length
                                 Copyright
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                                                                                                                    Run on:
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No.
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MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLJ
THERAPEUTIC PURPOSES
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COMPUTER: IEDOPY disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INPORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30, 024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECRAMINICATION INPORMATION:
US-09-166-448-81

US-09-705-160-44

US-09-705-160-44

US-09-440-621-3

US-09-440-621-6

US-09-440-621-6

US-09-440-621-8

US-09-440-621-10

US-09-440-621-10

US-09-440-621-10

US-09-440-621-10

US-09-440-621-10

US-09-697-884-81

US-09-697-884-81

US-09-697-884-81

US-09-697-884-81

US-09-697-884-81

US-09-697-884-80

US-09-697-884-81

US-09-697-884-81

US-09-751-798-5

US-09-751-798-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-979-847B-170
; Sequence 170, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
BEDIN, FREDERIC
; BEDIN, FREDERIC
; PARANNOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSES: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO: 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8 amino acids
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
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REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7356
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-032-848C-20
                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: BOX2' US-09-632-570-38
                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                3 LMIW 6
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Mitchinson, Colin
APPLICANT: Phillips, Jay Ian
TITLE OF INVENTION: No. 6623949e1 Variant EGIII-Like Cellulase
TITLE OF INVENTION: Compositions
FILE REFERENCE: GC631
CURRENT APPLICATION NUMBER: U$/09/632,570
CURRENT FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08032848C
Sequence 20, Application US/08032848C
Patent No. 5473101
GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Larenas, Edward
APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of TITLE OF INVENTION: Ed III Cellulase
NUMBER OF SEQUENCES: 20
                     52.1%; Score 25; DB 4; Length 8; 50.0%; Pred. No. 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 24; DB 4; Length 5; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,848C
FILING DATE: WAR 17 1993
CLASSIFICATION: 435
                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                 RESULT 2
US-09-632-570-35
; Sequence 35, Application US/09632570
; Patent No. 6633949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
                                     Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: BOX2
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1 TSOLTWIV 8
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US-08-032-848C-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 35
LENGTH: 5
                       Query Match
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Sequence 170, Application US/08635886C
Patent No. 6555114
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: MARTHENS, Geert
TITLE OF INVENTION: UMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT PILING DATE: 1994-10-28
PRIOR PILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-11-04
PRIOR FILING DATE: 1993-11-04
                                                Gaps
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APPLICANT: Mitchinson, Colin
APPLICANT: Mitchinson, Colin
APPLICANT: Philips, Jay Ian
TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
TITLE OF INVENTION: Compositions
FILE REFERENCE: GC631
CURRENT APLICATION NUMBER: US/09/632,570
CURRENT FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 644
SOFTWARE: FastEEQ for Windows Version 4.0
SEQ ID NO 38
                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
Length 6;
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50.0%; Score 24; DB 1; L
100.0%; Pred. No. 3.8e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                      Sequence 38, Application US/09632570 Patent No. 6623949
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ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: LEROUIX-ROELS, GEERT
DELEYS, ROBERT
MAERTENS, GEERT
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
SOFTWARE: PERCENTE R. 10, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-No. 6689368-1997
CLASSIFICATION: «Unknown»
ATTORNEY/ARBATION: «Unknown»
ATTORNEY/ARBATION: THOMAGE: REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NO. 6689368-1997
CLASSIFICATION: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-08-974-685-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 180:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE F
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-974-685-180
; Sequence 180, Application US/08974685
Patent No. 6689368
; GENERAL INFORMATION:
                                                                                                                                                                                                                              TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 170: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 180:
                                                                                                                                                                                                                                                                                                     LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAERTENS, GEERT
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
                                                                                                                                                                                      ;;
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Patent No. 661333

GENERAL INFORMATION:
PAPLICANT: LEROUX ROELS, Geert
APPLICANT: LEROUX ROELS,
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE OF INVENTION: VIRUS
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT PILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin Version 3.1
SEQ ID NO 170
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STATE: VIRGINIA
COMPUTRY: U.S.A.
ZIF: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRS: IBM PC compatible
COMPUTRS: PC - DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 4; Length 7;
Pred. No. 3.8e+05;
0; Mismatches 2; Indels
                                                                                                                                          Length 7;
                                                                                                                                        Score 24; DB 4; Pred. No. 3.8e+05;
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 170, Application US/08974685
Patent No. 6689368
GENERAL INFORMATION:
APPLICANT: LEROUIX-ROELS, GEERT
DELEYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
                                                                                                                                     Similarity 66.7%;
4; Conservative
                                            TYPE: PRT; ORGANISM: hepatitis C virus US-08-635-886C-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-170
                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                              4 MIWIMM 9
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US-08-974-690C-170
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US-08-974-685-170
  SEQ ID NO 170
LENGTH: 7
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Sequence 169, Application US/08979847B

Sequence 169, Application US/08979847B

Patent No. 6582703

GENERAL INFORMATION:

BESEME, FREDERIC

BEDIN, FREDERIC

BEDIN, FREDERIC

BENIAND-PRADEL, FLORENCE

JOLIVET-REYNAUD, COLETTE

MANDRAND, BERNARD

GARSON, JERENY

TUKE, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLA

THERAPEUTIC PURPOSES
         APPLICANT: SINITSYN, ARKADY PANTELEIMONOVICK
APPLICANT: BURSEN, MARTINE
APPLICANT: BOUSSON, JEAN CHRISTOPHE
APPLICANT: PANNONEN, CHRISTINE MARIE
APPLICANT: PUNT, PETER JAN
APPLICANT: PUNT, PETER JAN
APPLICANT: VAN.ZEIJL, CORNELIA MARIA JOHANNA
TITLE OF INVENTION: TRANSFORMATION SYSTEM IN THE FIELD OF FILAMENTOUS FUNGI
CURRENT APPLICATION NUMBER: US/09/548,938A
CURRENT APPLICATION NUMBER: 2000-04-13
SOFTWARE: PATENTING DATE: 2000-04-13
SOFTWARE: PATENTIN Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: AUNCHON-
NAME: BERRIDGE, WILLIAM P.
RECISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPHONE: 703-836-6400
TELEPHONE: 703-836-787
INFORMATION FOR SEC ID NO: 169:
SEQUENCE CHARACTERIFICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 24; DB 4; Length 8; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSES: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
OLSON, PHILIP TERRY
                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Chrysosporium sp.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LMIW 6
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US-08-979-847B-169
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                                                                                                                                                                                                                                                                                   SEQ ID NO 17
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Balent No. 5977440

GENERAL INFORMATION:

APPLICANT: LUTHE, DAWN S.

APPLICANT: BINGHUA, JIANG

APPLICANT: PECHAN, TIBOR

TITLE OF INVENTION: PROTEINASE AND ITS USE IN TRANSFORMING PLANTS TO PROVIDE TITLE OF INVENTION: INSECT RESISTANCE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: OBLON. SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                          Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,314C
FILING DATE: 30-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: RELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/POCKET UNBER: 2343-045-27
TELECOMMUNICATION:
TELEPHONE: 703-413-3000
                                        50.0%; Score 24; DB 4; I
66.7%; Pred. No. 3.8e+05;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: P.C.: JTSS S. JEFFERSON DAVIS HIGHWAY ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 17, Application US/09548938A Patent No. 6573086 ; Patent No. 6731086 ; GENERAL INFORMATION: APPLICANT: EMALFARB, MARK AARON APPLICANT: BURLINGAME, RICHARD PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Conservative
                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
                                          Query Match
Best Local Similarity
                                                                                                                              4 MIWIWM 9
                                                                                                                                                                         MANDMM 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SLMIW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:|
1 SVMVW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-09-548-938A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
US-08-974-685-180
                                                                                                                                                                                                                                        RESULT 9
US-08-641-314C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-641-314C-7
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                                                                                 Matches
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-258-754-385
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                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN UMBER OF SEQUENCES: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 4; Lengin >; Pred, No. 3.8e+05; 2; Indels
                                                                                                              Length 8;
                                                                                                          Score 24; DB 4; Pred. No. 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                             1; Mismatches
                 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-08-979-847B-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                            US-08-466-601A-160
; Sequence 160, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 29-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGIGSTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 421792
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
STRANDEDNESS: single
                                                                                                        Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 345 PARK AVENUE
NEW YORK
NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
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TSQLTWT 8
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MAWDWM 9

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APPLICANT: Ragualini, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
Sequence 40, Application US/08134231C;
Patent No. 6562596;
GENERAL INFORMATION:
APPLICANT: S1biger, Scott M.
KOSIL, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type;
TITLE OF INVENTION: Three (TIMP-3) Composition and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,231C
FILING DATE: 06-Occ-1993
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 22; DB 3; Length 7; ilarity 60.0%; Pred. No. 3.8e+05; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 4; 1
Pred. No. 3.8e+05;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: P-LJ 3443
CURENT APPLICATION NUMBER: US/09/258,754
CURENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
FEARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SEQ ID NO 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                    CITY: Washington
STATE: District of Columbia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 385, Application US/09258754; Patent No. 6174687; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                       NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserva
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Search completed: November 14, 2004, 14:08:30 Job time : 36 secs

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58, Appl 35, Appl 35, Appl 75, Appl 78, Appl 55, Appl 96, Appl 96, Appl 151, Appl 21, Appl 22, Appl 35, Appl 35, Appl 36, Appl 37, Appl 37, Appl 37, Appl 38, Appl 38, Appl 37, Appl 38, Appl 38, Appl 38, Appl 38, Appl 38, Appl 38, Appl 39, Appl 31, Appl 31, Appl 31, Appl 31, Appl 32, Appl 31, Appl 32, Appl 33, Appl 34, Appl 35, Appl 36, Appl 36, Appl 37, Appl 37, Appl 38, Appl 38

Sequence Seq

Sequence Sequence Sequence

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THILE OF INVENTION: 186 Human Secreted proteins
THILE OF INVENTION: 186 Human Secreted proteins
THILE OF INVENTION: 186 Human Secreted proteins
CURRENT REPERENCE: PC002P1
CURRENT PILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 615
EARLIER APPLICATION NUMBER: 60/047, 615
EARLIER PILING DATE: 1997-05-23
US-08-390-156A-58
US-08-390-156A-87
US-08-439-817-35
US-08-439-817-35
US-08-439-817-78
US-08-485-508-95
US-08-485-508-95
US-08-485-508-95
US-09-428-0828-151
US-09-180-100-25
US-09-632-570-35
US-09-632-570-38
US-09-632-570-38
                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 551, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-149-476-551
     Sequence 551, App
Sequence 50, Appl
Sequence 61, Appl
Sequence 22, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 50, Appl
Sequence 61, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 61, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                  November 14, 2004, 11:57:26; Search time 7.08511 Seconds (without alignments) 84.242 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2 6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-149-476-551

US-08-241-054-50

US-08-241-054-61

US-08-390-156A-22

US-08-390-156A-61

US-08-439-817-30

US-08-439-817-30

US-08-439-817-30

US-08-439-817-30

US-08-439-817-30

US-08-485-508-50

US-08-485-508-50

US-08-485-508-50

US-08-485-508-50

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US-08-247-155-20

US-08-247-155-20

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US-08-241-154-81

US-08-241-154-81

US-08-241-054-95

US-08-241-054-95

US-08-241-054-95

US-08-241-054-95

US-08-241-054-95

US-08-241-054-95
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                                                                                                                                                                                                                                                                                                                                   478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
                                                                                                                                                                                                   US-09-831-253F-5
48
                                                                                                                                                                                                                                       1 TSLMIWIMM 9
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Match Length
                                    Copyright
                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 23
                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB E
Maximum DB E
                                                                                          OM protein
                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
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R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R PILING DATE: 1997-04-11
R PILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,569 A APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
A APPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,613
R FILING DATE: 1997-05-23 A APPLICATION NUMBER: 60/047,582
R FILING DATE: 1997-05-23
A APPLICATION NUMBER: 60/047,596
R APPLICATION NUMBER: 60/047,612
R APPLICATION NUMBER: 60/047,612
R FILING DATE: 1997-05-23 LING DATE: 1997-04-11 PLICATION NUMBER: 60/043,312 ILING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 LING DATE: 1997-08-22 PLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 ILING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 ILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 PLICATION NUMBER: 60/047,587 LING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/056,877 PPLICATION NUMBER: 60/056,903 PPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/043,580 APPLICATION NUMBER: 60/056,886 APPLICATION NUMBER: 60/056,880 LING DATE: 1997-08-22 LING DATE: 1997-08-22 .997-08-2 ILING DATE: 1997-08-2 LING DATE: 1997-08-2 EARLIER 1 EARLIER SARLIER SARLIER EARLIER SARLIER

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,894

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,911

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,636

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,874

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,874

R FILING DATE: 1997-08-22 R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

R APPLICATION NUMBER: 60/056,892

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/057,761

R APPLICATION NUMBER: 60/047,595

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,590

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,589

R APPLICATION NUMBER: 60/047,589 R FILING DATE: 1997-08-22 R PELLING DATE: 1997-08-22 R PELLING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,875 R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,862 R FILING DATE: 1997-08-22 NG DATE: 1997-04-11 ICATION NUMBER: 60/047,501 NG DATE: 1997-05-23 ICATION NUMBER: 60/043,670 NG DATE: 1997-04-11 APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 LING DATE: 1997-08-22 PLICATION NUMBER: 60/056,876 PLICATION NUMBER: 60/056,887 LING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22
APPLICATION WUMBER: 60/056,864
ELING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,631 LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,585 LING DATE: 1997-05-23 PLICATION NUMBER: 60/047,593 LING DATE: 1997-04-11 PLICATION NUMBER: 60/043,576 CATION NUMBER: 60/056,632 IG DATE: 1997-08-22 LING DATE: 1997-05-23 PLICATION NUMBER: 60/047,614 CATION NUMBER: 60/043,578 CATION NUMBER: 60/056,664 CATION NUMBER: 60/056,881 LING DATE: 1997-08-22 LING DATE: 1997-05-23 EARLIER BARLIER BEARLIER BEARL EARLIER I EARLIER I EARLIER I EARLIER BARLIER BARLIER BEARLIER BEARLI EARLIER BARLIER EARLIER EARLIER EARLIER EARLIER PRLIER SARLIER SARLIER

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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwerla, Steven E.
APPLICANT: Marian, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swart-
FITHE OF INVENTION: STREET: 699 Prince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSER: Burns, Donne, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STREET: 699 Prince Street
CITY: Alexandria
CITY: Alexandria
CITY: Alexandria
COUNTRY: USA
ZIB: 22313
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
RIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1993
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION INFORMATION:
TELEPROME 415-854-7400
TELEFRAX: 415-854-7400
TELEFRAX: 415-854-770
                                                                                                                                                                     Sequence 53, Application US/08241054;
Patent No. 5643873;
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-241-054-61
; Sequence 61, Application US/08241054
; Patent No. 5643873
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Best Local Similarity 80.0
Einea 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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STRANDEDNESS: si
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MLWNMM 11
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7 LWTMM 11
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APPLICANT: William J.
APPLICANT: Koller, William J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
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                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/02/1,054
FILING DATE: 11-MAY-1994
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATORNEY/AGENT INFORMATION:
NAME: GGFald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 06-MAY-1902
TELEPHONE: 415-854-7400
TELEPHONE: 415-854-7400
                                                                                                                                                 58.3%; Score 28; DB 42.9%; Pred. No. 66; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                    EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50, Application US/08241054
Patent No. 5643873
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barrett, Ronald W. APPLICANT: Owirla, Steven E. Owirla, Steven E. APPLICANT: Dower, William J. APPLICANT: Koller, Kerry J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 12 amino acids
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Best Local Similarity
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-241-054-50
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US-08-39 D-158-AP D-1
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Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                        COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

REDICATION NUMBER: US/08/390,156A

FILING DATE: OF-MAX-1993

PRIOR APPLICATION NUMBER: US 07/881,395

FILING DATE: OF-MAX-1992

APPLICATION NUMBER: US 07/881,395

FILING DATE: OF-MAX-1992

APPLICATION NUMBER: SW189, 395

RIGHT ON NUMBER: SW189, 395

RESISTRATION: NUMBER: 30,113

RESISTRATION NUMBER: 30,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%;
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-08-390-156A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 MLWNWM 11
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                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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                                                                                                    APPLICANT: Loc, Malliam J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, June
APPLICANT: Lee, June
APPLICANT: Lee, June
APPLICANT: Mattens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothellum Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCE: 169
CORRESPONDENCE ADDRESS: 169
ADDRESSEBE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STRATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cavirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
TITLE OF INVENTION: Peptides and Compounds That Bind to NUMBED OF ENVIRONMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 12; 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/ASENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELLEPHONE: 415-854-7400
TELLEPHONE: 415-854-1875
INFORMATION FOR SEO ID NO: 61:
SEQUENCE CHARACTERISTICS:
CHARACTERISTICS:
CHARACTERISTICS:
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1; Mismatches
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Pred. No.
                                        Ronald W
                                                                            Cwirla, Steven E. Dower, William J.
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-241-054-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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US-08-390-156A-22
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APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Belectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
NUMBER OF SEQUENCES: 209
                                                                                                                                                                               Gaps
                                                                                                                                                                               ö
                                                                                                                              Score 28; DB 1; Length 12;
Pred. No. 72;
1; Mismatches 0; Indels
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Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPLY disk
COMPUTER: INDAPY disk
COMPUTER: INDAPY disk
COMPUTER: INDAPC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/21,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/21,054
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: US 07/881,395
FILING DATE: OF-MAY-1993
APPLICATION NUMBER: US 07/881,395
FILING DATE: APPLICATION NUMBER: LAURENTION:
NAME: SIEVENS, LAURENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000324-046/1056.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Affymax Technologies, NV
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/08439817
Patent No. 5728802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrett, Ronald W.
Cwirla, Steven E.
Dower, William J.
                                                                                                                                 58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4001 Miranda Ave
                                                                                                      Ouery Match
Best Local Similarity 80.0
              STRANDEDNESS: single
                                                     , MOLECULE TYPE: peptide US-08-390-156A-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity
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US-08-390-156A-61
; Sequence 61, Application US/08390156A
; Patent No. 5.48458
; GENERAL INFORMATION:
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dawrett, Ronald W.
; APPLICANT: Martens, Christine L.
; TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: ELAM-1
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 28; DB 1; Length 12; 80.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
FILING DATE: 16-FBB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATCHING DATE: 06-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Affymax Technologies, N.V.
PRICHING DATE: 05-WAY-1993
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/881,395
FILING DATE: 06-WAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REFERENCE/DOCKET WUMBER: 1023.1A
TELEPHONE: 415-496-2300
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-424-0832
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
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REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-230
TELEPHONE: 415-424-0332
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLYMBA Technol
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
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Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Betides and Compounds That Bind
ITILE OF INVENTION: Peptides and Compounds That Bind
ITILE OF INVENTION: Molecule I (BLAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ann.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 1; Length 12;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: RADAPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTONNEY/AGENT INPORMATION:
WAND: ACCOUNT OF TANKATION:
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                            US-08-439-817-41
; Sequence 41, Application US/08439817
; Patent No. 5728802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTYMAX Technol
CITY: Palo Alto
STATE: California
CONTRY: USA
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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Best Local Similarity
Matches 4; Conserv
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7 LWTMM 11
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US-08-485-508-50
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Bouler, Walliam J.
APPLICANT: Martens, Christine L.
APPLICANT: Christine L.

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       Gape
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Pred. No. 72;
1; Mismatches 0; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ENOPRY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 06-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATPORNEY/AGENT INPORMATION:
NAME: ADMINISTREMENTON:
       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERNCE/DOCKET NUMBER: 000324-046/1056.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
   1; Mismatches
                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/08439817
Patent No. 5728802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Affymax TechnoloSTREET: 4001 Miranda Ave. CITY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 33:
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80.0%;
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LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 4; Conservative
4; Conservative
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Barret
                                                                                                                                       6 MLWNWM 11
                                                                4 MIWIWM 9
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   Matches
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Gaps

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Lee, Jung
Martens, Christine L.
Rubland-Fritsch, Beatrice
RWHDION: Peptides and Compounds That Bind
VENTION: Selectins Including Endothelial Leukocyte Adhesion
VENTION: Molecule I
Selectins Including Endothelial Leukocyte Adhesion Molecule I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION NUMBER: US/08/485,508
FILING DATE: Herewith
RICASSIFICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 36,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 72;
1; Mismatches
TITLE OF INVENTION: Selectins Includir
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Affymax Technologies, NV 4001 Miranda Ave.
                                                                                                                                                                                                                   CITY: Palo Alto
CITY: California
COUNTRY: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett, Ronald W.
Cwirla, Steven E.
Dower, William J.
Koller, Kerry J.
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CORRESPONDENCES: 162
ADDRESSEE: Affymax Techno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

// MOLECULE TYPE: peptide

US-08-485-508-53
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7 LWTMM 11
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APPLICANT:
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                                   APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland Fritsch Beatrice
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF INVENTION: Molecule I
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Koller, William J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Rathens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 05-MAY-1993
ATPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTONREY/AGENT INFORMATION:
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4001 Miranda Ave.
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Patent No. 5786322
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stevens, Lauren L.
REGISTRATION UNDRER: 36,691
REFERENCE/DOCKET NUMBER: 0003;
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-496-2300
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
   Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 4001 Mirar
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%; Score 27; DB 3; Length 21; 57.1%; Pred. No. 1.8e+02; tive 3; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.2%; Score 27; DB 3; Length 21; Best Local Similarity 57.1%; Pred. No. 1.8e+02; Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09247155A
Patent No. 6312922
| GRUERAL INDORMATION:
| APPLICANT: Dumas Milne Edwards, Jean-Baptiste
| APPLICANT: Duclert, Aymeric
| APPLICANT: Bougueleret, Lydie
| TITLE OF INVENTION: Complementary DNAs
| FILE REFERENCE: GENSET.021A
| CURRENT APPLICATION NUMBER: US/09/247,155A
| CURRENT APPLICATION NUMBER: 06/074,121
| EARLIER APPLICATION NUMBER: 60/081,563
| EARLIER PILING DATE: 1998-02-09
| EARLIER FILING DATE: 1998-04-13
| EARLIER FILING DATE: 1998-04-13
| EARLIER FILING DATE: 1998-04-13
| EARLIER PILING DATE: 1998-04-13
| EARLIER RELING DATE: 1998-04-13
| EARLIER RELING DATE: 1998-04-13
| EARLIER RELING DATE: 1998-04-13
| SARLIER PILING DATE: 1998-10-04
| NUMBER OF SEQ ID NOS: 182
| SEQ ID NO 20
| LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: sig_peptide
LOCATION: 1..21
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.5
OTHER INFORMATION: seq_SFLPSALVIWTSA/AF
US-08-905-223-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..21
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.5
OTHER INFORMATION: seq SFLPSALVIWTSA/AF
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: 18 TEAGLEON, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                  TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::|:|||
13 SALVIWT 19
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US-09-247-155-20
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Pred. No. 72;
1; Mismatches 0; Indels
                                                                                     ZIF: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATPONREY/AGENT INPORMATION:
AMARE: GENERAL INFORMATION:
ANAME: GENERAL INFORMATION:
AMAME: GENERAL INFORMATION:
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Sequence 20, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-426-2300
TELEPHONE: 415-426-0300
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 aning acids
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CITY: San Diego
STATE: California
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
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Best Local Similarity 80.0%;
Matches 4; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
       Palo Alto
California
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Search completed: November 14, 2004, 12:08:48 Job time: 8.08511 secs

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November 14, 2004, 11:57:25; Search time 26.0426 Seconds (without alignments) 123.973 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2000s:\* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

seq length: 0 seq length: 23

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	Query Match	Length	08	ΩI		
-	48	100.0	6		AAY93096	Aay93096 Transform	, E
7	48	100.0	9	ო	AAY92949	Aay92949 Transform	Ę
3	36.5	76.0	12	m	AAY92947	7	E
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9	35	72.9	12	m	AAY93009	6	E
7	35	72.9		m	AAY93010	0	E
80	31	64.6	18	4	AAB89123	Aab89123 HIV qp120	0
6	31	64.6		4	AAB89121	Aab89121 HIV qp120	0
10	31	64.6	18	4	AAB89122	Aab89122 HIV qp120	0
11	28	58.3	6	ω	ADK08459	9 Hume	ρ
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21	28	58.3	12	N	AAR86068	Aar86068 Anti-ELAM	Σ
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24	28	58.3	12	7	AAW26900	Aaw26900 ELAM-1 b	bi
25	28	58.3	12	~	AAW26865	Aaw26865 ELAM-1 b	bi

Aaw63875 ELAM-1 pe Aaw63886 ELAM-1 pe Aaw63878 ELAM-1 pe Aay17756 Tarqet si		Aam 5505 Human bun Aam 62500 Human bra Aay 93098 Transform Aay 92950 Transform		Abb32925 Peptide # Aam36386 Peptide # Abb27754 Human pep Abb18404 Protein # Aam66109 Human bon
AAW63875 AAW63886 AAW63878 AAX17756	ABU93298 ABB41629 AAM35422	AAM62500 AAY93098 AAY92950	ABU64837 ADK08116 ADK08482 AAM13980	ABB32925 AAM26386 ABB27754 ABB18404 AAM66109
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26 23 29	30 32 32	1 4 6 6 4 6 6	33 8 4 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 1 4 6 4 8

## ALIGNMENTS

Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis. Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors. Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Transforming growth factor inhibitory peptide P142. (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA. AAY93096 standard; peptide; 9 AA 98ES-00002465. 99WO-ES000375. (first entry) WPI; 2000-411935/35. Borras Cuesta F; WO200031135-A1. Homo sapiens, 23-NOV-1999; 24-NOV-1998; 08-NOV-2000 02-JUN-2000. AAY93096; RESULT 1

Disclosure; Page 31; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides ANY9245-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or disease, specifically cirrhosis
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                                                                                                                                                                                 Hepatotropic; antagonist; transforming growth factor betal; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transforming growth factor inhibitory peptide P54.
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Pred. No. 3.9;
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                     AAY92947 standard; peptide; 12 AA.
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                         Score 48; DB 3; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming growth factor inhibitory peptide #5.
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ilarity 100.0%;
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Cuesta F;
                                                                                                                                             1 TSLMIWTMM
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                     Sequence 9 AA;
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Length 12; Indels

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y9131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolypic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or betall of the collagen synthesis) encoding the peptides are used for treatment of liver
                                                                                     Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                                                                                                                                               Disclosure; Page 31; 86pp; Spanish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    expression systems) encoding the disease, specifically cirrhosis
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAV92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                  Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatotropic, antagonist, transforming growth factor betal, TGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor; liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                     Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
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Pred. No. 3.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               sequences of the factor or its receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 27; 86pp; Spanish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, specifically cirrhosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                          WPI; 2000-411935/35.
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                                        WO200031135-A1.
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Query Match Best Loc Matches 24-NOV-1998;

23-NOV-1999;

02-JUN-2000

Homo sapiens

08-NOV-2000

AAY93094;

RESULT 5

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Gaps

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Gaps

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Mismatches

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6; Conservative
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 Matches
                                                                                                 RESULT 8
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                                                                                                              AAB89123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides ANY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
           examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimecopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
                                                                                                                                                                                  Gaps
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                                                                                                                                                     DB 3; Length 12; 7.3;
                                                                                                                                                                                                                                                                                                                                                                                        growth factor inhibitory peptide P56.
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                                                                                                                                                                                0; Mismatches
                                                                                                                                                   72.9%; Score 35; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                       AAY93010 standard; peptide; 12 AA
                                                                                             disease, specifically cirrhosis
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                                                                                                                                                                                  Conservative
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                                                                                                                                                              Best Local Similarity
Matches 6: Conser
                                                                                                                                                                                                                              MIWTWM 11
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                                                                                                                          Sequence 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         Transforming
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                                                                                                                                                                                                                                                                            RESULT 7
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DB 3; Length 12; 7.3;

72.9%; Score 35; 100.0%; Pred. No.

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chemokine receptor; CD4; HIV; glycoprotein 120; gpl20; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                             Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.
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Pred. No. 60;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV gp120 protein binding peptide #214.
                                                                                                                                                                                                                                                                HIV gp120 protein binding peptide #216
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                                                                                                                                         AAB89123 standard; peptide; 18
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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Query Match

Query Match

Best Local Similarity

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3; Conserve
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                                                                     Query Match
Best Local Similarity
                                                                                                            TSLMIWIM
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                                                      Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                   05-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
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                                                                                         Matches
                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                    bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.
                                                                                                                                      Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.
                                                                                                                                                                                              present invention describes a number of peptides which are able to
                                                                                                                                                                                                                                                                                         Gaps
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60;
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Pred. No. 60;
2; Mismatches
                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                              HIV gp120 protein binding peptide #215
                                                                                                                                                                           Example 3; Page 42; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 42; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                         AAB89122 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                      64.6%;
62.5%;
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                                            25-AUG-2000; 2000WO-US023505
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                                                                                                                                                                                                                                                                                                          1 TSLMIWTM 8
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                                                                                                                                                                                                                                                     Sequence 18 AA;
         WO200116182-A2.
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                                                              27-AUG-1999;
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                           08-MAR-2001
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The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemoxine receptors CRS. CXCR4 and STR133, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogenic virus, alternative reading frame, antigenic determinant, virucide, vaccine, therapeutic agent, infection, HPV.
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Pred. No. 1.7e+06;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                4; Length 18;
                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                Score 31; DB
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus peptide #514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK08459 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Habel A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUL-2002; 2002AT-00001124.
11-JUL-2003; 2003EP-00450171.
                                                                                                                                                                                                                                                      64.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2003; 2003WO-EP008112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattner F, Schmidt W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
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papilloma virus; childhood viral encephalitis; wart.
                                           WO2004002404-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004003145-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens,
                                                                08-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI46844;
                                                                                                                                                  Quay SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI46844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                    reading frame of a parhogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present
                                                                                                                                                                                                                                                                                                                                                a pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel polypeptide encoded by an alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                              frame; antigenic determinant;
infection; HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; permeabilising; interferon-beta; IFN-beta; mucosal delivery; immunosuppressive; virucide; autoimmune disease; viral disease; multiple sclerosis; chronic hepatitis B; condyloma acuminata;
                                                                                                                                                                                                                                                                                                                                              New polypeptide encoded by an alternative reading frame of a pathr
virus comprising an antigenic determinant, useful for treating or
preventing an infection with the pathogenic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; UB c,
5. 1.7e+06;
5. 1.7e+06;
6. Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 58.3%; Score 28; DB 8; Length 9; Similarity 37.5%; Pred. No. 1.7e+06; 3; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human JAM-1 permeabilising peptide SEQ ID NO:425.
                                                                                                                              c virus; alternative reading vaccine; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 175; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG94446 standard; peptide; 10 AA.
                                                                                                         Human papillomavirus peptide #150.
                                          ADK08095 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                       Habel A;
                                                                                                                             pathogenic virus; alternative virucide; vaccine; therapeutic
                                                                                                                                                                                                                            24-JUL-2003; 2003WO-EP008112
                                                                                                                                                                                                                                                24-JUL-2002; 2002AT-00001124
11-JUL-2003; 2003EP-00450171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                     Schmidt W,
                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                                          WPI; 2004-169243/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|::||::
ALVLWTLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SLMIWIMM 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                  WO2004011650-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
                                                                                   06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2004
                                                                                                                                                                                                                                                                                                     Mattner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG94446;
                                                               ADK08095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
ADG94446
                      RESULT 12
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The invention relates to a novel stable pharmaceutical composition comprising one or more interferon (IFN)-beta compound(s) formulated for mucosal delivery to a mammalian subject in combination with one or more mucosal delivery to a mammalian subject to the composition following mucosal administration to the subject yields enhanced mucosal delivery of the one or more IFN-beta compound(s). A composition following immunosuppressive and virucide activity. The composition is useful for treating autoimmune diseases, viral disease, for alteviating one or more symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma acuminata, papilloma virus warts of the larynx or skin or childhood viral encephalitis in the subject without unacceptable adverse side effects. The composition can be delivered intranasally which reduces or eliminates compliance problems and side effects that attend delivery by injection. The sequences shown in AbG94022-Ap04810 represent permeabilising
                                                                                                                                                                                                                                                                                                                                                                                                               Stable pharmaceutical composition comprising interferon compound(s) formulated for mucosal delivery to mammalian subjects in combination with mucosal delivery-enhancing agent(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mucosal delivery; permeabilising peptide;
mucosal epithelial paracellular transport; epithelial junction;
sepithelial membrane adhesive protein; junctional adhesion molecule; JAM;
occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;
female sexual dysfunction; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 1.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                              Gupta M, De Meireles JC, Abd El-Shafy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Permeabilising peptide of human JAM-2 SeqID553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 425; 353pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI46844 standard; peptide; 10 AA.
18-JUN-2003; 2003WO-US019261.
                                                                              28-JUN-2002; 2002US-0393066P.
                                                                                                                                                            (NAST-) NASTECH PHARM CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%;
62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 62.5
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TSLKIWNV 10
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Search completed: November 14, 2004, 12:02:11 Job time : 28.0426 secs
                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   3 TSLKIWNV 10
                                                                                                                                                                                                                                                                                                                                                                                        1 TSLMIWIM 8
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                          physiology
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                         Composition comprising biologically active agent and permeabilizing peptide that reversibly enhances mucosal epithelial paracellular transport by modulating epithelial junctional structure and/or physiology in mammal.
                                                                                                                                                                                                                                      This invention relates to a novel composition comprising a biologically active agent and mucosal delivery-enhancing effective amount of permeabilising peptide that reversibly enhances mucosal epithelial paracellular transport by modulating epithelial junctional structure and/or physiology in a mammal. The agent of the invention inhibits homotypic binding of epithelial membrane adhesive protein chosen junctional adhesion molecule (JAM), occludin and claudin. The biologically active agent is effective for treatment of sexual dysfunction, for example male erectile sexual dysfunction or female sexual dysfunction. The present sequence is that of a permeabilising peptide of human JAM-2 which may be used during the production of the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anorectic; cytostatic; eating disorder; neuroprotective; nootropic; cachexia; intranasal composition; peptide YY; obesity; cancer; malnutrition; wasting, Alzheimer; disease; colon adenocarcinoma; panoreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia; junctional adhesion molecule 2; JAM-2; epithelial junction; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 28; DB 8; Length 10; 62.5%; Pred. No. 1.1e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Junctional adhesion molecule 2 (JAM-2) peptide segid 426.
                                                                                                                                                                                                             Disclosure; SEQ ID NO 553; 426pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP87021 standard; peptide; 10 AA.
24-JUN-2003; 2003WO-US019994.
                          28-JUN-2002; 2002US-0392512P.
                                                       (NAST-) NASTECH PHARM CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-2002; 2002US-00322266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-2002; 2002US-00322266
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.55,
Local Similarity 62.55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TSLKIWNV 10
                                                                                                              WPI; 2004-091087/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-478989/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TSLMIWIM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (QUAY/) QUAY S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004115135-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP87021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quay SC;
                                                                                 Quay SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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The invention describes an intranasal composition comprising peptide YY compound(s) formulated for mucosal delivery to a mammalian subject. Also described is a kit for treatment of a mammalian subject comprising the intranasal composition of peptide compond(s). The composition is used for treating obseity, cancer, or malnutrition or wasting related to cancer in the subject. It is used to alleviate Alzheimer's disease, colon adenocarcinoma, pencreatic adenocarcinoma, breast carcinoma, treatment and prevention of malnutrition resulting from iatrogenic causes or cachexia associated with advanced disease, or cancer cachexia in the subject. The composition alleviates the symptoms without unacceptable adverse side effects. This is the amino acid sequence of a human junctional adhlesion molecule 2 (JAM-2) that may be used in a composition of the invention to modulate epithelial junction structure and/or
Intranasal compositions for treating obesity, cancer, or malnutrition or wasting related to cancer, comprises peptide compound(s) formulated for mucosal delivery to mammalian subject.
                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 426; 86pp; English.
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Gaps ö

58.3%; Score 28; DB 8; Length 10; 62.5%; Pred. No. 1.18+02; tive 1; Mismatches 2; Indels

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; OTHER INFORMATION: Description of Artificial Sequence: binding peptide US-10-084-813-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
64.6%; Score 31; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||:|| :
11 TSLLIWVI 18
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US-10-084-813-237
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LENGTH: 18
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238, App
Sequence 425, App
Sequence 553, App
Sequence 551, App
Sequence 45075, A
Sequence 33702, A
Sequence 20, Appli
                                                                                                November 14, 2004, 12:03:21; Search time 21.2553 Seconds (without alignments) 149.815 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

1: /cgr2_6/ptodata/1/pubpaa/VSO7_PUBCOMB.pep:*
2: /cgr2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgr2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
4: /cgr2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgr2_6/ptodata/1/pubpaa/NSO7_NEW_PUB.pep:*
6: /cgr2_6/ptodata/1/pubpaa/NSO7_NEW_PUB.pep:*
7: /cgr2_6/ptodata/1/pubpaa/NSO8_NEW_PUB.pep:*
9: /cgr2_6/ptodata/1/pubpaa/NSO8_PUBCOMB.pep:*
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19: /cgr2_6/ptodata/1/pubpaa/USIOR_PUBCOMB.pep:*
           5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-004-813-236
US-10-084-813-237
US-10-084-813-238
US-10-662-425-425
US-10-661-953-553
US-10-10-322-266-426
US-09-031-551
US-09-331-551
US-09-39-76-2
US-09-864-761-33702
US-09-684-761-43702
US-09-693-190-20
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     1568699 segs, 353819137 residues
           GenCore version Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                            US-09-831-253F-5
48
                                                                                                                                                                                           1 TSLMIWTMM 9
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Match Length
                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                             Perfect score:
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31
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                                                                                                                                                                                                                                                                     Searched:
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                                                                                                    Run on:
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US-10-084-813-236
; Sequence 236, Application US/10084813
; Sequence 236, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REPERENCE: 215875
; CURRENT FILING DATE: 2002-02-27
; CURRENT FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
                                                                                                                                                        Sequence 657, App
Sequence 657, Appl
Sequence 173, Appl
Sequence 173, Appl
Sequence 151, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
                                                  Sequence 126, App
Sequence 17, Appl
Sequence 36057, A
Sequence 170, App
Sequence 170, App
Sequence 632, App
Sequence 657, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 202, App
Sequence 332, App
Sequence 30555, A
Sequence 45706, A
Sequence 10, Appl
Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 594, App
Sequence 896, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 593,
                            14 US-10-231-452-7
10 US-09-953-354-126
19 US-09-953-354-126
19 US-09-964-761-36657
18 US-09-864-170
15 US-09-864-170
15 US-09-864-170
15 US-10-114-104-170
16 US-10-1182-252A-657
17 US-10-200-708-501
18 US-10-200-708-501
19 US-09-810-1851
19 US-10-60-217-151
19 US-10-20-218-151
19 US-10-20-218-151
19 US-10-20-218-151
19 US-09-217-18-19
19 US-09-217-18-19
19 US-09-217-18-19
19 US-09-217-18-19
19 US-09-217-18-19
19 US-09-217-18-19
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Gaps

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RESULT 6
US-10-322-266-426
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Sequence 237, Application US/10084813

Publication No. US20030068615A1

GENERAL INFORMATION:

APPLICANT: SAXINGER, CARL

TITLE OF INVENTION: POLYBEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

FILE REPERENCE: 215875

CURRENT PLING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US/10/084,813

PRIOR APPLICATION NUMBER: US/00/023505

PRIOR APPLICATION NUMBER: US 60/151,270

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SOFTWARE: PATENT VERSION 3.1

SEQ ID NO 237

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 238, Application US/10084813

Fublication No. US20030068615A1

GENERAL INFORMATION:

APPLICANT: SAXINGER. CARL

TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

FILE REFERENCE: 218875

CURRENT PLIJNG DATE: 2002-02-7

PRIOR APPLICATION NUMBER: US/10/084,813

CURRENT FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/151,270

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SOUTWARE: PATENT VERSION 311

SEQ ID NO 238

LENGTH: 18
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; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: binding peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%; Score 31; DB 14; Length 18; 62.5%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 62.5
Matches 5; Conservative
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7 TSLLIWVI 14
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US-10-084-813-238
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Sequence 553, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Unactional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Thrapeutic Compounds
FILE REFERENCE: 02-03US
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR SEQ ID NOS: 900
SOFTWARER: PatentIn version 3.2
SEQ ID NO 553
LENGTH: 10
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Publication No. US20040115135A1

GENERAL INFORMATION:

APPLICANT: Quay, Steven C.

TITLE OF INVENTION: YY And Methods For Enhanced Mucosal Delivery OF Peptid.

TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity

TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity

CURRENT APPLICATION NUMBER: US/10/322,266

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 797

SEQ ID NO 426
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## APPLICANT: Gupta, Malini
## APPLICANT: de Meireles, Jorge
## TITLE OF INVENTION: Compositions and Methods for Enhanced
## TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
## TITLE OF INVENTION: THE REFERENCE: 02-0208
## CURRENT APPLICATION NUMBER: US/10/462,452
## CURRENT PILING DATE: 2003-06-16
## PRIOR FILING DATE: 2003-06-28
## NUMBER OF SEQ ID NOS: 790
## SOFTWARE: FastSEQ for Windows Version 4.0
## SEQ ID NO 425
## LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
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Pred. No. 2.2e+02;
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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; OTHER INFORMATION: Synthetic construct
US-10-601-953-553
                                                                                                                                                                                                                                                                                                                                                                                                                        58.3%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.5%,
3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 62.5
Matches 5; Conservative
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CORGANISM: Homo sapiens
US-10-462-452-425
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R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,334
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,336
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,163
R APPLICATION NUMBER: 60/040,600
R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-03-07
                                                                                                                                                                                       R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,633
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
APPLICATION NUMBER: 60/047,592
APPLICATION NUMBER: 60/047,592
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
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APPLICATION WUMBER: 60/647,587
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-05-23
APPLICATION UNDBER: 60/047,598
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,632
FILING DATE: 1997-05-23
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APPLICATION WUMBER: 60/043,580
ELING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,583
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,311
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LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEX: SITE
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 551, Application US/0980391
Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICAMT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
                                                                                                                 Query Match 58.3%; Score 28; DB 16; Length 10; Best Local Similarity 62.5%; Pred. No. 2.2e+02; Matches 5; Conservative 1; Mismatches 2; Indels
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1) Sequence 551, Application US/09882171

CENTRAL INFORMATION: 1

APPLICANT: Ruben et al. 1

TITLE OF INVENTION: 186 Human Secreted proteins FILE REFRENCE: PZ002P2 CURRENT APPLICATION NUMBER: US/09/882,171 CURRENT FILING DATE: 2001-06-18 PRIOR APPLICATION NUMBER: 09/809,391 PRIOR APPLICATION NUMBER: 09/149,476 PRIOR FILING DATE: 1998-03-08 PRIOR FILING DATE: 1998-03-08 PRIOR FILING DATE: 1998-03-06 PRIOR FILING DATE: 1998-03-06 PRIOR FILING DATE: 1998-03-06 PRIOR FILING DATE: 1997-03-07 PRIOR APPLICATION NUMBER: 60/040,162 PRIOR FILING DATE: 1997-03-07                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                              ) OTHER INFORMATION: Synthetic construct US-10-322-266-426
              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 42.9
Matches 3; Conservative
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1 LLLWTLL 7
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LENGTH: 11
                                                 FEATURE:
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R APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-04-11
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/056,886
RR APPLICATION NUMBER: 60/056,886
RR APPLICATION NUMBER: 60/056,886
RR APPLICATION NUMBER: 60/056,897
RR PILING DATE: 1997-08-22
RR PELLANTION NUMBER: 60/056,899
RR FILING DATE: 1997-08-22
RR PELLANTON NUMBER: 60/056,899
RR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
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APPLICATION NUMBER: 60/056,903
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,880
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,761
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APPLICATION NUMBER: 60/056,882
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APPLICATION NUMBER: 60/056,637
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APPLICATION NUMBER: 60/056,879
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APPLICATION NUMBER: 60/056,894
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,864
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PPLICATION NUMBER: 60/056,631
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APPLICATION NUMBER: 60/056,845
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APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-08-22
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NAME/KEY: SITE
1 LOCATION: (11)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-164-861-551 LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids Gaps ö Score 28; DB 10; Length 11; Pred. No. 2.4e+02; 4; Mismatches 0; Indels APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P200219.
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PatentIn Ver. 2.0 PRIOR APPLICATION NUMBER: 60/043,578
PRIOR FILING DATE: 1997-04-11
PRIOR PILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,576
PRIOR APPLICATION NUMBER: 60/043,670
PRIOR APPLICATION NUMBER: 60/036,632
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR PILING DATE: 1997-04-11
PRIOR PILING DATE: 1997-06-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,875
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-25
PRIOR PILING DATE: 1997-08-25
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-27 Sequence 551, Application US/10164861 Publication No. US20030225248A1 GENERAL INFORMATION: 58.3%; Query Match Best Local Similarity 42.9 Matches 3; Conservative TYPE: PRT ORGANISM: Homo sapiens FEATURE: NAME/KEY: SITE 3 LMIWTMM 9 US-10-164-861-551 SEQ ID NO 551 LENGTH: 11 ò 셤

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Sequence 33702, Application US/09864761
; Sequence 33702, Application US/09864761
; Patent No. US20020048763A1
; Patent No. US2020048763A1
; Patent No. US2020048763A1
; Patent No. US2020048763A1
; APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Hank, David K.
APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
: CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-06-26
PRIOR PELING DATE: 2000-06-26
PRIOR PELING DATE: 2000-06-26
; PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN PLACENIA, SIGNAL = 0.47
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.46
OTHER INFORMATION: EST_HUMAN HIT: AW026680.1, EVALUE 9.00e-06
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PAPLICATION NUMBER: PCT/US01/00662
PRIOR PAPLICATION NUMBER: PCT/US01/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
PURKETH: 21
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Best Local Similarity 75.v
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 45075, Application US/09864761

patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-04

PRIOR PILING DATE: 2000-09-04

PRIOR PILING DATE: 2000-09-04

PRIOR PILING DATE: 2000-09-04

PRIOR APPLICATION NUMBER: US 60/23,366

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Sequence 2, Application US/09939769

PUBLication No. US20030017149A1

GENERAL INFORMATION:

APPLICANT: HOEFFLER, JAMES P.

APPLICANT: HOEFFLER, MARIJANE

TITLE OF INVENTION: SINGLE CHAIN ANTIBODY FUSION REAGENTS THAT REGULATE

TITLE OF INVENTION: TRANSCRIPTION IN VIVO

FILE REFERENCE: 039322/0226

CURRENT FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: 08/28,890

PRIOR FILING DATE: 1996-10-10
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Illustrative CTHER INFORMATION: mitochondrial target signal US-09-939-769-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%; Score 28; DB 10; Length 20; 33.3%; Pred. No. 4.3e+02; ive 4; Mismatches 2; Indels
                                        Length 11;
                                                                                               0; Indels
                                        Score 28; DB 14;
Pred. No. 2.4e+02;
                                                                                               Mismatches
                                     58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                               3; Conservative
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                                  Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                3 LMIWIMM 9
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dunda Mille Edwards, Jean-Baplible
APPLICANT: Dunda Mille Edwards, Jean-Baplible
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.034.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR PILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 10; Length 21;
Pred. No. 6.6e+02;
3; Mismatches 0; Indels
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Pred. No. 6.68+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, Jean-Baptiste
                                                                                                                                                                                                                                  LOCATION: 1..21
OTHER INFORMATION: VON Heijne matrix
OTHER INFORMATION: SCORE 5.5
OTHER INFORMATION: SEQ SFLPSALVIWTSA/AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: SCORE 5.5
OTHER INFORMATION: SEQ SFLPSALVIWTSA/AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-864-761-45706
; Sequence 45706, Application US/09864761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10319763
Publication No. US20030144490A1
GENERAL INFORMATION:
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57.1%; Pred
3;
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Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
NUMBER OF SEQ ID NOS: 182
                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapiens
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13 SALVIWT 19
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13 SALVIWT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TSLMIWT 7
                           SOFTWARE: Patent.pm
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SIGNAL LOCATION: 1..21
                                                                                                                                                                                                    NAME/KEY: SIGNAL
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                                                                                    LENGTH: 21
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APPLICANT: Dumas mile Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-13
PRIOR PILING DATE: EARLIER RILING DATE: 1998-08-10
PRIOR PILING DATE: EARLIER PILING DATE: 1998-08-10
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N: EXPRESSED IN H9144, SIGNAL = 0.89

N: EXPRESSED IN HBL100, SIGNAL = 0.74

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3

N: EXPRESSED IN HELA, SIGNAL = 0.89

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.7

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

N: EXPRESSED IN HEART, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB 9; Length 20;
Pred. No. 6.3e+02;
2; Mismatches 1; Indels
               PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
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Publication No. US20030162176A1
PUBLERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%;
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Best Local Similarity 57.1
Matches 4; Conservative
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LENGTH: 20
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PARTERAL INTO WINGWATION

PARTICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Harkel, David R.

ANDORSEN: ADMINISTICAL STORNER: US/09/864,761

CURRENT FILING DATE: 2001-02-03

PRIOR RELING DATE: 2001-02-04

PRIOR RELING DATE: 2000-03-04

PRIOR PRIOR PRICATION NUMBER: PCT/USO1/0663

PRIOR RELING DATE: 2000-03-04

PRIOR PRICATION NUMBER: PCT/USO1/0663

PRIOR PRICATION NUMBER: PCT/USO1/0661

PRIOR PRIOR PCT/USO1/0661

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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.6
US-09-864-761-45706
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Patent No. US20020048763A1
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ORGANISM: Homo sapiens
FEATURE:
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Search completed: November 14, 2004, 12:26:59 Job time : 21.2553 secs

10 TRLEIWNMI 18

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Agas57877 influenza P92689 podospora a Q93140 neisseria m Q91434 myxococcus 019454 mus musculu 025012 helicobacte Q9nz62 homo sapien 085406 coxiella bu Q8nhl3 homo sapien Q7rpe0 plasmodium 077896 oreochromis

perga conde influenza a

Q6q1m2

Q9zyv8 aspilota

Scoring table:

Searched:

Database

Result Š. Perfect score: Sequence:

Run on

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Nakanishi Y.;
"Transcription Stimulaton of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection.";
[2]
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                              Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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MEDLINE=98355401; PubMed=7543095;
Mada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
Nakanishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
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Pred. No. 8.1e+02;
3; Mismatches 1; Indels
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Matiasovic J., Horin P.;
Submitted (FB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF354453; AAK43589.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       21 AA; 2259 MW; A064CFFD5F9A71E4 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last seque
01-ULJ-2004 (TrEMBLrel. 27, Last annol
Fas antigen (CD95 antigen) (Fragment)
        Q9ZYX7
Q6QLM2
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Q93TW0
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09NZ62
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42.9%;
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7 TTYLVWT 13
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Matches 3; Conserv
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QBr5g1 spermophilu
QBiv5s home sapien
QBo074 human herpe
P3403 acman herpe
QBBC home sapien
P3287 lactococcus
QBBC chamaeleo
P1370 jarropha mu
QBBK chamaeleo m
QBM19 influenza a
QGQIM influenza a
QGQIM influenza a
Aas57979 influenza a
Aas5799 influenza a
Aas5799 influenza a
Aas5799 influenza a
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09uel0 homo sapien
06ldl9 rattus norv
Aaa41680 rattus no
06lea8 xenopus lae
Aaa49911 xenopus l
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                                                                       November 14, 2004, 11:57:26; Search time 24.0319 Seconds (without alignments) 215.479 Million cell updates/sec
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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DCAM ACACA
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QBSHF6
Q6WRB2
AAQ23391
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Maximum Match 100%
Listing first 45 summaries
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Q6LDL9
AAA41680
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BAA00902
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AAS57880
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Q9ESU5
Q7S3Q9
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Q9NZ61
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Q6QLL7
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq
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Gaps

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Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                           MEDLINE-Sprague-Dawley,
MEDLINE-90287121; PubMed=1694009;
Chen A., Reyes A., Akeson R.A.;
"Transcription initiation sites and structural organization of the extreme 5' region of the rat neural cell adhesion molecule gene.";
Mol. Cell. Biol. 10:3314-3324(1990).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L26396; AAA49911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 17 AA; 2026 MW; AEA1EB5F252E84F5 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Neural cell adhesion molecule (Fragment).
Name=NCAM;
     02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Neural cell adhesion molecule (Fragment).
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Last annotation update)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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"Transcription initiation sites and structural organization of the streme S. region of the rat neural cell adhesion molecule gene.";
Mol. Cell. Biol. 10:3314-3324 [1990].
EMBL, M32612; AAA41680.1;
                         Muschen M., Re D., Brauninger A., Wolf J., Hansmann M.L., Diehl V.,
Kuppers R., Rajewsky K.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 MEDILINE-22404279; PubMed=12516573;
A Kurth J., Perniok A., Schmitz R., Iking-Konert C., Chiorazzi N., Andmongon K.M., Winkler T., Rajewsky K., Kueppers R.;
I. Lack of deleterious sometic mutations in the CD95 gene of plasmablasts from systemic lupus erythematosus patients and autoantibody-producing cell lines.";
L. Bur. J. Immunol. 32:3785-3792(2002).
R. EMBL; AJ279011; CAC35539.1; -. REMBL; AJ279011; CAC35540.1; -. REMBL; AJ279011; CAC35540.1; -. REMBL; AJ279011; CAC35541.1; -. REMBL; AJ279011; CAC36541.1; -. REMBL; AJ279011; CAC36541.1; -. REMBL; AJ209180; CAD48930.1; -. REMBL; AJ209180; CAD48930.1; -.
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Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Neural cell adhesion molecule (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=90287121; Pubmed=1694009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.1%;
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50.0%;
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Best Local Similarity 50.0
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                                                                                                                                       SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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AAA41680;
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                                                                                                  Squire T.L., Andrews M.T.; "Pancreatic triacylglycerol lipase in a hibernating mammal. I. Novel genomic organization.";
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MEDLINE=20127858; PubMed=10660538;
MURDLINE=20127858; PubMed=10660538;
MURDLINE=20127858; PubMed=10660538;
MURDLINE=20127858; P.; Bourdon J.C., Nagata S., May E.,
Yonish-Rouach E., Reisdorf F.;
"Human and mouse Fas (APO-1/CD95) death receptor genes each contain
p53-responsive element that is activated by p53 mutants unable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 2.3e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                              Score 23, DB 2; Length 15;
Pred. No. 2.1e+03;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                          C6F85151A7050414 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 24, Last annotation update)
Fas death receptor (Fragment)
Mus musculus (Mouse).
                                                                                                                                                       Physiol. Genomics (Online) 16:119-130(2003).
EMBL; AY071823; AAL73074.1; -.
NON_TER 15 15
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Matches 2; Conservative
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Name=STEERIN2;
Homo sapiens (Human).
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SEQUENCE FROM N.A.
                                          SEQUENCE FROM N.A.
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    NCBI_TaxID=43179;
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                                                                                  PubMed=14583598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.

MEDLINE=22096038; PubMed=12099803;

Howarth D.G., Baum D.A.;

"Phylogenetic utility of a nuclear intron from nitrate reductase for the study of closely related plant species.";

Mol. Phylogenet. Evol. 23:525-528(2002).

EMBL. AF460205; ALG6737.1; ---

GO; GO:0016491; Floxidoreductase activity; IEA.

InterPro; IPR005066; Mo-co_dimer.

Pfam; PF03404; Mo-co_dimer; 1.
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                                                        SEQUENCE FROM N.A.
Johnson A.D., Ovesnek N., Tonissen K.F., Krieg P.A.;
"The Xenopus NCAM promoter: Appropriate expression in response to neural inducing signals and identification of a conserved sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermophilus tridecemlineatus (Thirteen-lined ground aquirrel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Spermophilus.
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                                                                                                                                      element.";
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L26396; AAA49911.1; -.
NON TER 17 17 ....
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pancreatic triacylglycerol lipase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nitrate reductase (Fragment).
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nes 3; Conservative
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Xenopodinae; Xenopus
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7 LIWTL 11
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                     NCBI_TaxID=8355;
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Viruses, dsDNA viruses, no RNA stage, Herpesviridae,
Alphaherpesvirinae, Simplexvirus.
NCBI_TaxID=10298;
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Best Local Similarity
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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

A Jaffe D., Fitzhugh W., Ma L.J., Smirnov S., Purcell S., Rehman B.,

A Jaffe D., Fitzhugh W., Man S., Nielsen C.B., Buller J., Endrizzi M.,

A Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,

A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

A Kothe G.O., Jedd G., Mawes W., Staben C., Marcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Maylor J., Thomann N., Barrett R., Gnerre S.,

RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catcheadde D., Li W., Pratt R.J., Osmani S.A.,

Basouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

A varden O., Plamann M., Seiler S., Dunlag J., Radford A., Aramayo R.,

RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
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-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HSV-1 glycoprotain C (Fragment).
Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 2; Length 17;
Pred. No. 5.4e+03;
3; Mismatches 0; Indele
                                                                                                                                                                                 Score 21; DB 2; Length 10;
Pred. No. 3.2e+03;
2; Mismatches 2; Indels
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ICE 17 AA; 2044 MW; 33C34BDEEAF0F3A2 CRC64;
                                                                                                                   10 10 10 10 10 10 AA; 1242 MW; 22145E32CDC37043 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          17 AA.
  induce apoptosis.";
J. Biol. Chem. 275:3867-3872(2000).
EMBL; AF282865; AAG02410.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                            Query Match
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Best Local Similarity 42.39,
Best Local Similarity
3, Conservative
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2 LWIWAVL 8
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1 MILWT 5
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CC -1- COFACTOR: Pyruvoyl group.

CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the anthopropyl moiety required for spermidine and spermine biosynthesis from putrescine.

C -1- SUBNITH: Heteroterramer of two alpha and two beta chains.

C -1- SUBNITH: Heteroterramer of two alpha and two beta chains.

C -1- SUBLOPMENTAL STAGE: Expressed only during exponential growth.

C -1- INDUCTION: Stimulated by putrescine. Inhibited by aromatic diamidines berenil, pentamidine, propamidine, hydroxystilbamidine, by ethidium bromide and methylglyoxal.

C -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

PER: S18763; S18763.
-i- FUNCTION: S-adenosylmethionine decarboxylase is essential for the biosynthesis of spermine and spermidine. The alpha subunit contains the active site.
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Hugo E.R., Byers T.J.;
"S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii
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05-JUL-2004 (Rel. 44, Last annotation update)
S-adenosylmethionine decarboxylase alpha subunit (EC 4.1.1.50)
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Plani, PR01536; SAM decarbox, 1.
PROSITE; PS01136; ADOMETDC; PARTIAL.
Decarboxylase; Direct protein sequencing; Lyase; Pyruvate;
                                                                                                                                                                                                                                                                                                    43.8%; Score 21; DB 2; Length 17; 12.5%; Pred. No: 5.4e+03; ative 7; Mismatches 0; Indels
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Pred. No. 6e+03;
3; Mismatches
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Acanthamoeba castellanii (Amoeba)
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Similarity 33.3%;
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Best Local Similarity 12.30,
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SEQUENCE FROM N.A.
MEDLINE=89166510; PubMed=3233219;
Umeno M., MeBride W.O., Yang C.S., Gelboin H.V., Gonzalez F.J.;
Umeno M., MeBride W.O., Yang C.S., Gelboin H.V., Gonzalez F.J.;
"Human ethanol-ineudible P450IIE1: complete gene sequence, promoter characterization chromosome mapping, and cDNA-directed expression.";
Biochemistry 27:9006-9013(1988).
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MEDLINE=95122459; PubMed=7529759;
Watanabe J., Hayashi S., Kawajiri K.;
Watanabe J., Hayashi S., Kawajiri K.;
"Different regulation and expression of the human CYP2E1 gene due to the Real polymorphism in the 5'-flanking region.";
J. Blochem. 116:321-326(1994).
BEMBL, D10014; BAA00902.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CYCOCHOME P450IIE1 (Fragment).

CYP2E1.

CYP2E1.

Euhen sapjens (Hunan).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome P450IIE1 (Fragment).
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MEDLINE=92138659; PubMed=1778977;
Hayashi S.;
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RX WEDLINE=89166510; PubMed=3233219;
RA Unenon M., McSride W.O., Yang C.S., Gelboin H.V., Gonzalez F.J.;
RT characterization chromosome mapping, and cDNA-directed expression.";
RI Biochemistry 27:9006-9013(1988).
RN Watunabe J. Hayashi S., Kawajiri K.;
RX MEDLINE=95122459; PubMed=7529759;
RA Watunabe J., Hayashi S., Kawajiri K.;
RT "hifferent regulation and expression of the human CYP2E1 gene due to RT the RsaI polymorphism in the 5' -flanking region.";
RT This 3212459; PubMed=7529759;
RA Watunabe J., Hayashi S., Kawajiri K.;
RT This 3212459; PubMed=7529759;
RA Watunabe J., Hayashi S., Kawajiri K.;
RT This 3212459; PubMed=7529759;
RA Watunabe J., Hayashi S., Kawajiri K.;
RT The RsaI polymorphism in the 5' -flanking region.";
RT The RsaI polymorphism in the 5' -flanking region.";
RT This 3216(1994).
DR RWELL, DI0014; BAA00902.1; -..
FT NON TER 21
SQ SEQÜENCE 21 AA; 2175 MW; 60A85A2B034F339B CRC64;
Best Local Similarity 40.0%; Pred: No. 6.6e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 3; Li!!
Db 9 ALLVW 13
Search completed: November 14, 2004, 12:07:33
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 14, 2004, 11:57:25 ; Search time 5.55319 Seconds (without alignments) 155.938 Million cell updates/sec Run on:

US-09-831-253F-5 48 1 TSLMIWTMM 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

4495 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		do.			COLUMNIC	
Result No.	Score	Query	Query Match Length	DB	ΩĮ	Description
1	2	9	16	7	PH1638	Ig H chain V-D-d r
8	25	52.1	7	N	PX0008	glucuronosyltransf
Э	25	S	16	7	PH1637	Ig H chain V-D-J r
4		50.0	13	N	PH1636	×
S		47.9	13	~	PH1620	Ig H chain V-D-J r
9		47.9	14	7	PH1625	Ig H chain V-D-J r
7	23	47.9	14	~	PH1627	=
œ		47.9	15	~	PH1613	Ig H chain V-D-J r
6		47.9	15	7	PH1612	H chain
10	23		17	~	PH1630	Ig H chain V-D-J r
11		47.9	20	7	PH1358	Ig heavy chain DJ
12		45.8	14	N	A35105	hypothetical prote
13		43.8	14	~	PH1327	-C
		•	15	~	PH1590	b
15	21	•	20	~	PL0192	Ig lambda 2 chain
			20	~	S38763	denosy
17	20	41.7	14	~	PH1626	Ig H chain V-D-J r
			22	~	I58038	MHC class I transp
19	20	٠.	22	~	A64548	hypothetical prote
20		39.6	12	~	I58273	thyroglobulin - ra
21	19		15	~	PH0782	T-cell receptor al
22	19		17	~	PH1331	Ig heavy chain DJ
	19		18	7	I59649	human leukocyte an
24	19		19	7	A28702	ò
25	19		19	N	145957	protein kinase (EC
56	19	σ.	19	~	153673	amyloid protein -
27	19	39.6	19	7	PH1352	y chain
58	19	39.6	19	~	PH1315	Ig heavy chain DJ
53	19	39.6	19	~	140063	shikimate 5-dehydr

major outer membra cytochrome-c oxida	cold-inducible pro Iq heavy chain CDR	hypothetical prote Iq H chain V-D-J r	collecting duct wa	Ig H chain V-D-J r	leukotriene B-4 12 T-cell receptor be	Ig heavy chain CDR	L-lactate dehydrog photosystem I 8.0K	photosystem I prot hypothetical prote	
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30 31	33 33	34 35	36 75	38	8 4 0 0	41	4. 4. 2. E.	4.4. 5.	

## ALIGNMENTS

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RESULT 1
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PH1638

19 H chain V-D-J region (clone B-less 228) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: PH1638

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Residues: 1-16 cLEV

A;Residues: 1-16 cLEV

A;Residues: 1-16 cLEV

A;Residues: immunoglobulin

Query Match
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 2; Mismatches 1; Indels

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Gaps

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10 TTSMLWT 16 1 TSLMIWT 7 요 ò

# RESULT 2

PACORA PACORA PACORA By Alternate names: UDP-glucuronyltransferase C;Species: Ratus norvegicus (Norway rat) C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997 C;Accession: PX0008 R;Yokoca, H.; Yusas, A.; Sato, R. J. Biochem. 104, 531-536, 1988 R;Yokoca, H.; Purification and properties of a form of UDP-glucuronyltransferase from liver A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver A;Reference number: PX0008; MUID:89197852; PMID:3149280 A;Accession: PX0008 A;Molecule type: protein A;Residues: 1-7 <YOK> C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match
52.1%; Score 25; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels

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Gaps

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1 TSLMIW 6 1 TKLLVW 6 셤 ð

RESULT 3 PH1637

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PHIGOS.

IG H chain V-D-J region (clone B-less 109) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: PHIGOS

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic: A;Reference number: PHIS80; MUID:93301609; PMID:8315387

A;Accession: PHIGOS

A;Accession: PHIGOS

A;Accession: PHIGOS

A;Accession: PHIGOS

A;Residues: 1-14 <LEV>
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte

C;Reywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Final Chain V-D-J region (clone B-less 120) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1627
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Title: Mode. 178, 317-329, 1993
A;Title: Mode.ular characterization of transgene-induced immunodeficiency in B-less micraly Reference number: PH1580; MUID:93301609; PMID:8315387
A;Reference number: Lubs.
A;Residues: 1-14 < LEV>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Title: Molecular Characterization of transgene-induced immunodeficiency in B-less mic: A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1613
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Pred. No. 2.7e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: bone marrow pre-B lymphocyte C, Keywords: immunoglobulin
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A;Residues: 1-15 cLEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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Similarity 75.0%;
3; Conservative
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Matches 3; Conserv
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Ig H chain V-D-J region (clone B-less 226) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O2-Un-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHI637
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PHI580; MUID:93301609; PMID:8315387
A;Molecule type: DNA
A;Residues: 1-16 < LEV>
A;Residues: 1-16 < LEV>
A;Residues: landucal source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig H Chain V-D-J region (clone B-less 224) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PH1636
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1636
A;Accession: PH1636
A;Residues: 1-13 <LEV-
A;Residues: 1-13 <LEV-
A;Residues: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0.2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1620
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Reference number: DNA
A;Molecula type: DNA
A;Residues: 1-13 <-LEV
A;Residues: 1-13 <-LEV
A;Residues: 1-13 <-LEV
A;Residues: immunoglobulin
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Pred. No. 2.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 2; Length 16;
Pred. No. 1.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 13;
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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Best Local Similarity 75.0%;
Matches 3; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 75.0%;
Matches 3; Conservative
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10 MLWT 13
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hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: mitochondrion Neurospora crassa
C;Species: mitochondrion Neurospora crassa
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C;Accession: A35105
R;Saville, B.J.; Collins, R.A.
C=11 61, 685-696, 1990
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora A;Reference number: A35105
A;Accession: A35105
A;Accession: A35105
A;Accession: A35105
A;Accession: A5105
A;Accession:
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Ig heavy chain DJ region (clone C113-105) - human (fragment)

Species: Homo sapiens (man)

C;Dete: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1327

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymp

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1327
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IG H chain V-D-J region (wild-type clone 141) - mouse (fragment)

CjSpecies: Mus musculus (house mouse)

CjSpecies: Mus musculus (house mouse)

CjAccession: PHISSO

R,Levinson, D.A.; Campos-Torres, J.; Leder, P.

A,Exp..Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A,Reference number: PHISSO; MUID:93301609; PMID:8315387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.8%; Score 22; DB 2; Length 14; Best Local Similarity 40.0%; Pred. No. 4.1e+02; Matches 2; Conservative 3; Mismatches 0; Indels
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A;Residues: 1-15 <-LEV>
A;Residues: 1-18 c-LEV>
C;Keyperimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Genome: mitochondrion
A,Genetic code: SGC3
C,Keywords: mitochondrion
8 TTTTVWT 14
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4 LWTLL 8
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R. Levinson, D.A.; Campos-Torres, J.; Leder, P.
R. Levinson, D.A.; Campos-Torres, J.; Leder, P.
R. Levinson, D.A.; Campos-Torres, J.; Leder, P.
A. Title: Mode.ular characterization of transgene-induced immunodeficiency in B-less mice A; Reference number: PH1580; MUD:93301609; PMID:8315387
A; Recension: PH1630
A; Molecule type: DNA
A; Residues: 1-17 cLEV>
A; Experimental source: bone marrow pre-B lymphocyte
                                                                                                                 PH1612

19 H chain V-D-J region (wild-type clone 344) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Caccesion: PA1612

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

J. Exp. Med. 178, 317-329, 1993

J. Exp. Med. 178, 317-329, 1993

A;Ritler Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1358
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph A;Reference number: PH1302; MUID:93094761; PMID:1460419
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C;Species: Mus musculus (house mouse)
C;Date: (2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Residues: 1-15 -LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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A;Residues: 1-20 <WAS>
C;Keywords: heterotetramer; immunoglobulin
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Score 21; DB 2; Length 15; Pred. No. 6.8e+02;

43.8%;

Query Match Best Local Similarity

1 TSLMIWT 7

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Iglambda 2 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PL0192
R;Alonso, A.; Chang, L.A.; Murialdo, H.
Mol. Immunol. 27, 115-17, 1990
A) Mille: Analysis of the expression of murine lambda genes transfected into immunocompet A;Reference number: PL0192; MUID:90205873; PMID:2108323
A;Accession: PL0192
A;Accession: PL0192
A;Accession: L.A.
A;Residues: 120 (ALO)
C;Genetics:
A;Mille: Alonsolobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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Search completed: November 14, 2004, 12:03:12 Job time : 6.55319 Becs

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01-WAY-2000 (TYEMBLYE1. 13, L6
DexB (Fragment).
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PubMed=12368865;
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01-MAR-2004
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Query Match
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Q76mm5 eurypharynx
Bab81140 euryphary
Q7m154 bacillus th
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Q79a22 borrelia bu
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Carlton J.W., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
A Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
A Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
A Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
A Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cumingham D.A., Preiser P. R., Bergman L.W., Vaidya A.B.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
A Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
"Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
Nature 419:512-519 (2002)
C. -! - CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                      Plasmodium yoelii yoelii.
Bukaryotan Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
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                                                                                               Hypothetical protein (Fragment).
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Hypothetical protein.
NOM TER 9 9
SEQUENCE 9 AA; 1001 MW; 4687
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Last sequence update) Last annotation update)

10 AA

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Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-
"Scale Gene Rearrangements Originated Within the Bels.";
Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046477; BAB87140.1; -.
Mitcahondrion.
NON TER. 10 10
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                                                                                                                      NADH dehydrogenase subunit 2 (Fragment).
                                                                                                                                                                          Eurypharynx pelecanoides (pelican eel)
                                              02-MAR-2004 (TrEMBLrel. 27, Created)
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MEDLINE=22967687; PubMed=12949142;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
Evolution of the deep-sea gulper eel mitochondrial genomes: largescale gene rearrangements originated within the eels.";

Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eurypharynx pelecanoides (pelican eel).
Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 2; Length 12;
Pred. No. 1.2e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                         Iannelli F., Pearce B.J., Pozzi G.;
"The type 2 capsule locus of Streptococcus pneumoniae.";
J. Bacteriol. 181:2652-2654(1999).
                                         Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=D39;
Pearce B.J., Iannelli F., Pozzi G.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF026471; AAD10169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB046477; BAB87140.1, -
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.7%;
40.0%;
                            Streptococcus pneumoniae.
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Best Local Similarity 40.0
Matches 4; Conservative
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                                                                                                                                                SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=1313;
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Mitochondrion.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,
                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Parasporal crystal protein, wax moth-specific (Fragment).
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25, DB 2, Length 11;
Pred. No. 1.7e+03;
1, Mismatches 0; Indels
                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C6FF9BD64764444D CRC64;
PRT;
                                                                                                                                                                                                                                                                                                                                  entomocidal activity.";
FEBS Lett. 232:249-251(1988).
PIR; S00616; S00616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
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SEQUENCE 11 AA; 1237 MW;
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PRELIMINARY;
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NNPYS 9
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RESULT

RESULT 4 BAB87140

13 AA

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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=JCM4673 / KCC S-0673;
PubMed=9538199;
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50.0%;
                          Q79A22;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                               SEQUENCE 13 AA; 1484 MW;
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               PRELIMINARY;
                                                                                MoxR protein (Fragment).
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                                                                                                                                                                                           Old I.G.;
Submitted (FEB-1996)
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Best Local Similarity
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                                                                                                                                  NCBI_TaxID=139;
                                                                                               Name=moxR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=W-17, and W-50;
MEDLINE=22779048; PubMed=12897253;
Palaisa K.A., Morgante M., Williams M., Rafalski A.;
Palaisa K.A., Morgante M., Williams M., Rafalski A.;
"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1799-1806(2003).
EMBL; AX300592; AAP55331.1; -.
                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                             12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;
            ol-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nume-psy2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Phytoene synthase 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 2; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 2;
Pred. No. 2e+03;
1; Mismatches
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MEDLINE=22779048; PubMed=12897253;
                                                                                                                                                                                                                                                                                                                                                        33.3%;
54.5%;
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54.5%;
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                                                                                                NCBI_TaxID=4577;
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                                                                                                          Zea mays (Maize)
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SEQUENCE
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           07XB05
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Q7XB05
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ઠ 셤 RESULT 8

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Nishimura M., Matsuo H., Sugiyama M.;
"Blasticidin S-producing Streptomyces morookaensis possesses an enzyme activity with hydrolyzes puromycin.";
PEMS Microbiol. Lett. 132:95-100(1995).
-!- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL TEMPERATURE IS 45 DEGREES CELSIUS.
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BY REGULATION: STIMULATED BY DIT. STRONGLY INHIBITED BY ZINC
ION, FERROUS ION, CUBRIC ION, WERCURY ION, N-BROWOSUCCINIMIDE AND
N-ETHYLMALEIMIDE. PARTIALLY INHIBITED BY COBALT ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Niehimura M., Matsuo H., Nakamura A., Sugiyama M.; Matsuo H., Intification and characterization of a puromycin-hydrolyzing enzyme from blasticidin S-prodducing Streptomyces morookaensis."; J. Biochem. 123:247-252(1998).
                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Puromycin-hydrolyzi/ng enzyme (EC 3.-...) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C7C2DF4CFD83A046 CRC64;
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Aminopeptidase; Hydrolase.

NON TER. 14 14

SEQÜENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64
                               Last sequence update)
Last annotation update)
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Pred. No. 2.1e+03;
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Pred. No. 2e+03;
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Created)
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55.6%;
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1; Mismatches

Conservative

5,

Matches

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910160

RESULT 10

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SEQUENCE FROM N.A.
MEDLINE=22967687; PubMed=12949142;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
Iroue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the deep-sea gulper eel mitochondrial genomes: largescale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Burypharyngidae; Burypharynx.
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Pred. No. 3.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.; Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB046485; BAB87156.1; --
EMBL; AB046481; BAB87146.1; --
GO; GO:0005739; C:mitochondrion; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;
                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
                            10 AA
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                                                                                                                                                          NADH dehydrogenase subunit 2 (Fragment).
Name=ND2;
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                                                                                                                                                                                                               Eurypharynx pelecanoides (pelican eel)
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                            PRT;
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                         PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=55117;
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                      Q76MK9
Q76MK9;
05-JUL-2004
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BAB87148;
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BAB87148
Q76MK9
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STRAIN=A/Hong Kong/491/97;
STRAIN=A/Hong Kong/491/97;
Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
Subbarao K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=A/Hong Kong/503/97;
Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.
Subbarao K.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
10-DEC-2001 (TrEMBLrel. 19, Last annotation update)
11-DEC-2001 (TrEMBLRel. 19, Last an
                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nuclear export protein NS2 (Fragment).
Influenca A virus (A/Hong Kong/503/97(HsN1)).
Viruses; seRNA negative-strand viruses; Octhomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.0%; Score 24; DB 2; Length 8; 62.5%; Pred. No. 1.8e+06; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.0%; Score 24; DB 2; Length 8; 62.5%; Pred. No. 1.8e+06; cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF256191; AAK49324.1; -.
NON TER 1
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1es 5; Conservative
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                      3 PYSAFQVDI 11
                                                          1 SNPYSAFQ 8
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Best Local Similarity
Matches 5; Conserv
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NON\_TER SEQUENCE Query Match

Best Loc Matches

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Q91U21 Q91U21;

RESULT 11

NON TER NON TER SEQUENCE

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Gaps

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Gaps

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Query Match 30.7%; Score 23; DB 2; Length 10; Best Local Similarity 66.7%; Pred. No. 3.5e+03; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                        Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AB046489; BAB87164.1; -. Mitochondrion.
                                                                                                                                                                                                                                   NON TER 10 10 SQÜENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 14, 2004, 13:16:22 Job time : 101 secs
Mol. Biol. Evol. 20:1917-1924(2003)
                                                   SEQUENCE FROM N.A. STRAIN=D;
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"Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
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"Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
Scale Gene Rearrangements Originated Within the Eels.";
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Mitochondrion.
Mitochondrion.
Musayotas, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Burypharymgidae; Burypharynx.
10TB_TaxID=55117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Burypharyngidae; Burypharynx.
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                                                            Length 10;
                                                      h 30.7%; Score 23; DB 2; Length 10; Similarity 66.7%; Pred. No. 3.5e+03; 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO46485; BAB87156.1; -.
Mitochondition
   10 AA; 1293 MW; 356FAE29C682DB47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                      BAB87156 PRELIMINARY; PRT; 10 AA. BAB87156; 20-MAR-2004 (TrEMBLrel. 27, Created) 02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) NADH dehydrogenase subunit 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
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                                                Query Match
Best Local Similarity
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BAB87164;
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SEQUENCE
                                                                                                                   Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds Run on:

(without alignments)
78.723 Million cell updates/sec

US-09-831-253F-4 75 Perfect score:

1 SNPYSAFQVDIIVDI 15 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2523

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		40			SOMMERLES	
Result No.	Score	Ouery Match	Query Match Length	DB	ID	Description
-	25	33.3	11	2	800616	parasporal crystal
~	23	30.7	13	(7)	A54326	
٣	23	30.7	14	~	B44854	L-2,4-diaminobutyr
4	22	29.3	12	~	A61360	vespakinin M - hor
S	22	29.3	15	~	PS0185	27K protein A 3.4/
9	22	29.3	15	N	A61612	allatostatin - tob
7	22	29.3	15	~	G24417	interphotoreceptor
80	21	28.0	11	~	PT0229	Ig heavy chain CDR
σ	21	28.0	12	~	S36899	ribosomal protein
10	21	28.0	13	~	PC2369	unidentified 85K p
11	21	28.0	15	~	PA0061	protein QF200039 -
12	21	28.0	15	~	S29174	D-galactose-bindin
13	20	26.7		~	S10784	enamelin i - bovin
14	20	26.7	1	N	A59018	MUC1 enhancer bind
15	20	26.7	7	~	808209	hypothetical prote
16	20	26.7	-	N	PQ0778	NADH2 dehydrogenas
17	19	25.3		~	S36898	ribosomal protein
18	19	25.3	7	~	A40795	glycoprotein H-a -
19	19	25.3	1	N	865612	tubulin alpha-chai
20	19	25.3	1	~	G22565	R-phycoerythrin ga
21	19	25.3	1	~	PQ0700	unidentified 6.3/4
22	19	25.3	7	N	A28018	very late antigen-
23	19	25.3	14	~	S07768	soluble hydrogenas
24	18	24.0		~	D47393	neuropeptide calla
25	18	24.0	-	7	PT0250	Ig heavy chain CRD
26	18	24.0	12	~	S70344	amine oxidase (cop
27	18	24.0	13	~	B20907	Ig kappa-1 chain J
28	18	24.0	14	~	829209	avenin alpha-2 - o
29	18	24.0	14	~	T46634	acyl carrier prote

Pax-QNR, long form	Ig heavy chain DJ	porphobilinogen sy	alpha-glucosidase	hypothetical TEL/M	prealbumin - weste	MHC class I histoc	protein QA100052 -	Ig heavy chain C r	ornithine decarbox	proton-translocati	T-cell receptor be	bma protein - Clos	T-cell antigen rec	H+-transporting tw	hypothetical prote
B56884	PH1365	S62641	PT0090	138335	149404	JQ0914	PA0050	C39111	B33710	869123	PH0771	140663	S47361	S21247	PS0371
7	0	~	N	4	7	7	~	~	~	N	N	~	~	7	7
14	15	15	15	13	80	σ	10	10	10	12	12	12	13	14	14
24.0	24.0	24.0	24.0	24.0	22.7	22.7	22.7	22.7	22.7	22.7	22.7	22.7	22.7	22.7	22.7
18	18	18	18	18	17	17	17	17	17	17	17	17	11	17	17
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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paragoral crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria paragoral crystal protein, wax moth-specific - Bacillus thuringiensis
NyAlternate names: delta-endotoxin; parasporal crystal protein positive chain
Sybcies: Bacillus thuringiensis
C; bate: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C; Accession: 500616
R; Chestuchina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A; Pitle: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endoto:
A; Reference number: 500616
A; A; Accession: 500616
A; A; Accession: 500616
A; A; Costerior con control con control con
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Pred. No. 2.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%;
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Best Local Similarity 80.0
Matches 4; Conservative
RESULT 1
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:|||| NNPYS 9 1 SNPYS 5 Ŋ ð g

RESULT 2

A54326

glandular kallikrein-1 - human (fragment)

cjspecies Humo sapiens (man)

cjspecies 29-Aug-1994 #man (man)

cjspecies 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

cjbate: 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

CjAccession: A54326

R;Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J. Mol. Cell. Endocrinol. 76, 181-190, 1991

A;Title: Identification and androgen-regulated expression of two major human glandular A;Title: Identification and androgen-regulated expression of two major human glandular A;Reference number: A54326

A;Status; preliminary; not compared with conceptual translation

A,Molecule type: nucleic acid A,Residues: 1-13 «RIE» A,Residues: 1-13 «RIE» A,Experimental source: prostate A,Note: sequence extracted from NCBI backbone (NCBIP:108060)

Gaps ö Query Match 30.7%; Score 23; DB 2; Length 13; Best Local Similarity 80.0%; Pred. No. 6.8e+02; Matches 4; Conservative 1; Mismatches 0; Indels

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G.B.; Li, J.P.; Carney,

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RiFong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
ERSB Lett. 205, 309-312, 1986
A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
A;Reference number: A91365; MUID:86301171; PMID:3743780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain CDR3 region (clone 1-115) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0229
R;Yamada, M; Wasserman, R; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: A61612
R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Katacka, H.; Quistad, G.B.; Li, J.P.; Car Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
A;Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta. A;Reference number: A61612; MUID:92052112; PMID:1946359
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Manduca sexta (tobacco hornworm)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
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N;Alternate names: interstitial retinol-binding protein
C;Species: Cricetinae gen. sp. (hamster)
C;bate: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Accession: G24417
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C;Keywords: neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Pred. No. 1.2e+03;
0; Mismatches 2; Indels
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A,Residues: 1-11 <74M>
A,Experidental aource: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: G24417
A;Modecule type: protein
A;Residues: 1-15 <FON
A;Cross-references: UNIPROT:P12665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 29.3%;
Similarity 66.7%;
4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                         allatostatin - tobacco hornworm
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QVDIIVDI 15
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-15 <KRA>
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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7 FQPSLVLDM
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CiAccession: A61360
CiAccession: A61360
CiAccession: A61360
CiAccession: A61360
A; Title: Veppakinin-24, 2896-2897, 1976
A; Title: Veppakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ven A; Reference number: A61360; MUID:77114342; PMID:1017116
A; Accession: A61360
A; Accession: A61360
A; Accession: A61360
A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the ven A; Conserver of the containing hydroxyproline, in the containing hydroxypro
                                                                                                                                                                                                       L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - vibrio alginolyticus (fragment)
C;Species: Vibrio alginolyticus
C;Species: Vibrio alginolyticus
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B44884; B41817
G;Accession: B44884; Y: Tougou, K.; Shinoda, S.
A;Tile: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from A;Reference number: A44854; MUD:92381494; PMID:1512577
A;Accession: B44854
A;Acce
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995
C;Accession: PSO184
A;Accession: PSO184
A;Accession: PSO185
A;Accession: PSO186
A;A
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;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
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C;Keywords: hydroxyproline; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
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Pred. No. 7.4e+02;
2; Mismatches 0; Indels
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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TAFEVD 7
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Sun Nov 14 13:50:56 2004

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Deglactose-binding lectin III - Axinella polypoides (fragment)
Cispecies: Axinella polypoides
Cipate: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
CiAccession: 829174
Ribuck, F.; Luth, C.; Strupat, R.; Bretting, H.
Ribuck, F.; Luth, C.; Strupat, R.; Bretting, H.
Ribuck, F.; Comparative ints9; 18, 1992
A;Title: Comparative investigations on the amino-acid sequences of different isolectins
A;Reference number: $29172; MUID:93003351; PMID:1390906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enamelin i - bovine (fragment)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cibate: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
CiAccession: 810784
Ristrawich, E.; Glimcher, M.J.
Ristrawich, E.; Glimcher, M.J.
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is alba A;Reference number: 810780; MUID:90336641; PMID:2379503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AS9018

WICL enhancer binding protein 70K chain MUCIEBP-70 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

C;Accession: A59018

E;Abe, M.; Smith, C.J.; Larson, C.J.

Bubmitted to the Protein Sequence Database, May 1998

A;Description: Involvement of "Ku-like" proteins in the transcription of MUCI/DF3, a br

A;Reference number: A59018
                              Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.0%; Score 21; DB 2; Length 15; 20.0%; Pred. No. 1.8e+03; tive 7; Mismatches 5; Indels
                                                                                Indels
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                           Score 21; DB 2; I
Pred. No. 1.8e+03;
2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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A;Molecule type: protein
A;Residues: 1-9 <STR>
A;Cross-references: UNIPROT:Q7M2M7
C;Keywords: enamel; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: P28588
                              28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SNPYSAFQVDIIVDI 15
                              Query Match 28.0
Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                     5 SAFQVDIIVD 14
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A;Molecule type: protein
A;Residues: 1-15 <BUC>
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                                                                                                                                                                                                                                                                                      Fibosomal protein S6 - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Saccession: S3689
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac A;Reference number: S36899
A;Accession: S3689
A;Accession: S3689
A;Accession: S3689
A;Accession: S3689
A;Accession: S3689
C;Keywords: proliminary
A;Molocule type: protein
A;Residues: 1-12 cOHA>
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A. submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotrich
A;Reference number: PA0051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Bacillus cereus
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: PC23569
R;Matenno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 211-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulation A;Reference number: PC2369; MUID:95218265; PMID:7766022
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Score 21, DB 2; Length 11;
Pred. No. 1.3e+03;
2; Mismatches 2; Indels
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A,Residues: 1-15 <CHO>
A,Cross-references: UNIPROT:Q7M4Y2
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  28.0%;
38.5%;
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Best Local Similarity 50.۰۰
است میرادی
                                                                                                         2 NPYSAFQVDIIVD 14
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Matches 3; Conservative
                                                       Conservative
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A;Molecule type: protein
A;Residues: 1-13 <MAS>
                           Best Local Similarity
Matches 5; Conserv
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8 NPWAKF 13
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     Query Match
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Gaps

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RESULT 15
508209
hypothetical protein 2 - garden pea
N.Alternate names: phytochrome
C;Species: Pisum sativum (garden pea)
C;Species: Pisum sativum (garden pea)
C;Accession: 508209
R;Sato, N.
Plant Mol. Biol. 11, 697-710, 1888
A;Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: di
A;Reference number: 508209
A;Accession: 508209
A;Accession: 508209
A;Residues: 1-15 <SAT>
A;Cross-references: EMBL:X14077; NID:g20836; PID:g20838
C;Genetics:
A;Gene: phy
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                                                             Query Match 26.7%; Score 20; DB 2; Length 14; Best Local Similarity 33.3%; Pred. No. 2.5e+03; Matches 3; Conservative 3; Mismatches 3; Indels
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26.7%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels
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A;Note: 3-Val was also found
C;Keywords: DNA binding; heterodimer
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RESULT 1
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                                                                                                     November 14, 2004, 12:55:26 ; Search time 93.3333 Seconds (without alignments) 57.653 Million cell updates/sec
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                2002273 seqs, 358729299 residues
   GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
geneseqp2000s:*
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geneseqp2002s:*
geneseqp2003as:*
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geneseqp2004s:*
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75
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### H. pylori H. pylori Transform Transform Transform Transform Transform pylori Liver : PTP1B | PTP1B Human Human Human BCFV Description Aay92951 Aay93059 Aay93069 Aay93067 Abp55430 Abr75594 Ad170905 Ad170907 Ad170906 Ad170906 Ad170907 Ad170908 Ad297913 Ad297913 Aab89867 I Aab89868 I Aab89868 I Aab89866 I Aab89866 I Adh48572 I ADN07473 ADL70819 ADL70905 ADL70907 AAY93067 ABP55430 ADL70906 ADL70908 AAG66403 ABP47086 AAY93099 AAY93059 AAB86060 ADG97913 DB Query Match Length 441.3 440.0 440.0 440.0 338.7 37.3 Score Result No.

res pho pho pho pho vas

VHCD

HIV gp120 HIV gp120 HIV gp120 ATP-depen

AAB89867 AAB89868 AAB89866 ADH48572

Transform

Abp46828 Human BLy	Adg97655 scFV VHCD		Aab89913 HIV gp120		Aab89917 HIV gp120	Aab89912 HIV gp120	Aab89915 HIV gp120	Abr01397 Human ant	Adc44449 Endotheli	Aar67117 Anti-infl	Aam97539 Human pep	Aar97882 Japan ced	HIV	Aab89681 HIV gp120	Aab89678 HIV gp120	Aab89679 HIV gp120	Aab89674 HIV gp120	Aab89673 HIV gp120	Aab89680 HIV gp120
ABP46828	ADG97655	AAB89916	AAB89913	AAB89914	AAB89917	AAB89912	AAB89915	ABR01397	ADC44449	AAR67117	AAM97539	AAR97882	AAB89677	AAB89681	AAB89678	AAB89679	AAB89674	AAB89673	AAB89680
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36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92245-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis. Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors. Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F; Transforming growth factor inhibitory peptide #4. (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA Ź Claim 5; Page 81; 86pp; Spanish. AAY92948 standard; peptide; 15 98ES-00002465. 99WO-ES000375 (first entry) WPI; 2000-411935/35. WO200031135-A1 Homo sapiens. 23-NOV-1999; 24-NOV-1998; 08-NOV-2000 02-JUN-2000 AAY92948; 

Query Match

X S

Matches

AAY93066;

RESULT 2 AAY93066

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial anino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                        Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor inhibitory peptide P145.
                                                                                                                                                   Transforming growth factor inhibitory peptide #7.
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Pred. No. 2.8e-05;
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                     AAY92951 standard; peptide; 14 AA
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Best Local Similarity 85.77,
Best Local Similarity 15.77,
Conservative
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                                                                                                                                                                                                                                                                                                                       WO200031135-A1.
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                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                             AAY92951;
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AAY92951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                         Gaps
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                                                             Length 15;
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                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor inhibitory peptide P106.
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                                                               Score 75; DB 3; I
Pred. No. 3.9e-07;
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                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                   AAY93066 standard; peptide; 15
                                                           Match 100.0%;
Local Similarity 100.0%;
les 15; Conservative 0
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les 15; Conserv
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Length 14;

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                               Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 28; 86pp; Spanish.
                                                                                                                                                                   Disclosure; Page 28; 86pp; Spanish
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  Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ezquerro Saenz I.
Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                         Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatotropic, antagonist, transforming growth factor betal; TGF-b1, competitive inhibition, collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                                                                                                                                                                                                                   Lasarte Sagastibelza JJ, Prieto Valtuena J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 3; Length 14;
Pred. No. 2.8e-05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor inhibitory peptide P105.
                                                                                                                                                                                                           (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 31; 86pp; Spanish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.78;
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                                                                                                                                                                                                                                                 Saenz IJ,
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les 12; Conserv
                                                                                                                                                                                                                                                                         Borras Cuesta F;
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                                       WO200031135-A1.
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Homo sapiens.
                                                                                                                         23-NOV-1999;
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Best Loc Matches

RESULT 5 AAY93059

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ABR75594 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                       subject sample.
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                                                                     28-AUG-2003
                                                                                                                                                                                                 08-MAY-2003.
                                                                                                                                                     Synthetic.
   RESULT 8
ABR75594
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those of TGF-b1 and/or its receptors. Peptides ANY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel human breast susceptible gene coded protein 10.45 polypeptide, and the polynucleotide encoding it, useful for treating several diseases e.g. embryotic development deformity and tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes human breast susceptible gene coded protein 10.45 (I). Also described is a process for preparing (I) using DNA recombination techniques. (I) can be used for treating several diseases e.g. embryotic development deformity and tumours. The present sequence represents the N-terminal peptide of (I), which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                           Human breast susceptible gene protein 10.45 N-terminal peptide SEQ:7.
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                  Human; breast susceptible gene coded protein 10.45; tumour;
                                                                                                                              Length 15;
                                                                                                                           62.7%; Score 47; DB 3; Length 15;
100.0%; Pred. No. 0.078;
ive 0; Mismatches 0; Indels
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Pred. No. 84;
4; Mismatches
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                                                                                                                                                                                                                                                         ABP55430 standard, peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                              embryotic development deformity.
                                                                                disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2000; 2000CN-00125173
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                                                                                                                           Query Match 62.7
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                         1 AFQVDIIVDI 10
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Best Local Similarity
Matches 5; Conserv
                                                                                                      Sequence 15 AA;
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                                                                                                                                                                                                                                                                              ABP55430;
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The present invention describes a method (MI) for screening or diagnosing a liver response in a subject, determining the stage or severity of a liver response in a subject, identifying a subject at risk of developing liver response, or monitoring the effect of therapy administered to a subject having liver response, involving detecting liver response.

Could be associated protein isoforms (LMRIS) (see the peptides given in ABR75395 to ABR75806) in a test biological sample from the subject, or monitoring the screening or diagnosing a liver response in a subject, or monitoring the screening or diagnosing a liver response in a subject, or monitoring the consecutive nucleotides complementary to a nucleotide sequence encoding consecutive nucleotides complementary to a nucleotide sequence encoding with cDNA copied from the RNA, where the contacting occurs under conditions that permit hybridisation of the probe to the nucleotide sequence, and comparing the hybridisation, if any, detected in the above steep, with the hybridisation detected in a control and ample or with a previously determined reference range. Mi su seeful for ample or with a previously determined reference range. Mi su useful for ample or with a previously determined reference range. Mi su useful for ample or with a previously determined reference range. Mi su useful for ample or with a previously determined reference range. Mi su useful for any and comparing the subject or with a previously determined reference range.
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                                                                                        Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:332.
                                                                                                                                                                             Biomarker; liver response; liver response-associated protein isoform;
LRPI; liver response-associated feature; LRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening, diagnosing, staging or identifying subject at risk of developing, liver response, or monitoring effect of therapy on liver response, by detecting Liver Response-Associated Protein Isoforms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stiger TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 6; Length 15;
Pred. No. 84;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy administered to a subject having liver response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holt GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herath HMAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PFIZ ) PFIZER PROD INC. (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 66; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002; 2002WO-US034847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2001; 2001US-0335964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.3%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amacher DE, Fasulo LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 YSAFQVDIIVD 14
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Best Local Similarity
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RESULT 9 ADN07473

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Gaps

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Indels

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5, Conservative

SPYFKFRVNVI 15 2 NPYSAFQVDII 12

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ADL70819 standard; peptide; 15 AA.

RESULT 10

ADL7081

2 YPGSQLDILID 12

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(first entry)

03-JUN-2004

ADL70819;

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response in a subject, determining the stage or severity of a liver response in a subject, dentifying a subject at risk of developing liver response, or monitoring the effect of therapy administered to a subject having liver response. The method involves detecting liver Response. Associated protein Isoforms (LRPIS) in a test biological sample from the subject, which has an activity or level indicative of a liver response. LRPIS are selected from any one of the compounds given in the specification e.g. LRPI-1.1, LRPI-2.1, LRPI-3.1 and LRPI-4.1 a subject, or monitoring the effect of a drug or therapy administered to a subject, or monitoring the effect of a drug or therapy administered to a subject, or more consecutive nucleotides complementary to a nucleotide sequence encoding an LRPI with RNA obtained from a biological sample from the nucleotides complementary to a nucleotide sequence conditions that permit hybridisation of the probe to the nucleotide sequence, and comparing the hybridisation detected in a control sample, or with a previously determined reference range. The method is cueful for screening or diagnosing a liver response in a subject, determining the stage or severity of a liver response, and subject at risk of developing liver response, and control sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of screening (M1) or diagnosing a liver
                                                                                                                                    liver response; liver response-associated protein isoform; LRPI;
drug monitoring; therapy monitoring; liver response-associated feature;
LRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening, diagnosing, staging or identifying subject at risk of developing, liver response, or monitoring effect of therapy on liver response, by detecting Liver Response-Associated Protein Isoforms in subject sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herath HMAC, Holt GD, Stiger TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 7; Length 15;
Pred. No. 84;
3; Mismatches 3; Indels
                                                                                                          Liver response-associated feature LRF405 #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 332; 75pp; English.
ADN07473 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                         31-OCT-2002; 2002US-00285394
                                                                                                                                                                                                                                                                                                                                                             31-OCT-2001; 2001US-0335964P
                                                                        (first entry)
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feature (LRF) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amacher DE, Fasulo LM,
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HERATH H M A C.
                                                                                                                                                                                                                                                                                                                                                                                                  AMACHER D E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-430566/40.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOLT G D.
                                                                                                                                                                                                                                                      US2003228583-A1
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                                                                                                                                                                                                                  Homo sapiens.
                                                                        17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                (AMAC/)
(FASU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STIG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (HERA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOLT/)
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Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor; phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity; inflammation; multiple sclerosis; angiogenesis-dependent disease; infectious disease; appetite suppressor; congestive heart failure; neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to phosphopeptides that inhibit protein tyrosine phosphatase. The phosphopeptides are useful as a medicament of for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity, inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used for preventing or treating congestive heart failure, neurodegenerative diseases, ischaemic events of the brain or demyalinating diseases. The present sequence is one such phosphopeptide from protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New phosphopeptides that inhibit protein tyrosine phosphatases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
                                                                                                                             Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hooft Van Huijsduijnen R, Walchli S, Arigoni F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                                                                                     /note= "Phosphotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 17; 77pp; English.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                          PTP1B phosphopeptide, SEQ ID 17.
                                                                                                                                                                                                                                           protein tyrosine phosphatase 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2003; 2003WO-EP050385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2002; 2002EP-00019357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphatase 1B (PTP1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-269210/25.
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YNAYQVD 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                               Synthetic
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Gaps

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sequence of a liver response-associated

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5; Conservative

Matches

41.3%;

ADL70905

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Cardiant, Neuroprotective, Protein tyrosine phosphatase inhibitor, phosphopeptide; protein tyrosine phosphatase; cancer, diabetes; obesity, inflammation; multiple sclerosis; angiogenesis-dependent diaesse; infectious disease; appetite suppressor; congestive heart failure;
                   Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor; phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity; inflammation; multiple sclerosis; angiogenesis-dependent disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used for preventing or treating congestive heart failure, neurodegenerative diseases, ischaemic events of the brain or demyelinating diseases. The present sequence is one such phosphopeptide from protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to phosphopeptides that inhibit protein tyrosine phosphatase. The phosphopeptides are useful as a medicament of for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity, inflammation, multiple sclerosis, anglogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e.
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                                                                                       infectious disease; appetite suppressor; congestive heart failure; neurodegenerative disease; prplB;
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Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV
                                                                                                                                                                                                                                                                             /note= "Phosphotyrosine"
                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1; 77pp; English.
                                                                                                                                        protein tyrosine phosphatase 1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2003; 2003WO-EP050385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2002; 2002EP-00019357.
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71.4%;
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Modified-site
                                                                                                                                                                                      Synthetic
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Matches
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à
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                                                                                                                                                                                                                               Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor; phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity; inflammation; multiple sclerosis; angiogenesis-dependent disease; infectious disease; appetite suppressor; congestive heart failure; neurodegenerative disease; ischaemia; demyellnating disease; PTPIB; protein tyrosine phosphatase 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to phosphopeptides that inhibit protein tyrosine phosphatese. The phosphopeptides are useful as a medicament or for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity, inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used for preventing or treating congestive heart failure, neurodegenerative diseases, ischaemic events of the brain or demyelinating diseases. The phosphatase 18 (PTP1B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
                                                                                                                                                                                                         Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
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                 ADL70905 standard; peptide; 15 AA.
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                                                                                                               (first entry)
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                                                                                                                                                              PTP1B phosphopeptide #19
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9 YNAYQVD 15
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Best Local Similarity
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                                                                                                             03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                 ADL70905;
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor; phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity; inflammation; multiple sclerosis; angiogenesis-dependent disease; infectious disease; appetite suppressor; congestive heart failure; neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
                                                                                                                                                                                                                                                                                                                                                The present invention relates to phosphopeptides that inhibit protein tyrosine phosphatase. The phosphopeptides are useful as a medicament or for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity, inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used for preventing or treating congestive heart failure, neurodegenerative diseases, ischaemic events of the brain or demyelinating diseases. The present sequence is one such phosphopeptide from protein tyrosine
                                                                                                                                                                                                                                                                  New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic, Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%; Score 30; DB 8; Length 15; 71.4%; Pred. No. 1.3e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                       Hooft Van Huijsduijnen R, Walchli S, Arigoni F;
                                                                                                                                                                                                (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV
                                                                              /note= "Phosphotyrosine"
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL70908 standard; peptide; 15 AA.
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             protein tyrosine phosphatase 1B
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                                                                                                                                                  20-AUG-2003; 2003WO-EP050385
                                                                                                                                                                         29-AUG-2002; 2002EP-00019357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 71.4%;
nes 5; Conservative
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                                                                                                      WO2004020466-A1
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Modified-site
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                                   Synthetic.
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Matches
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Human; vascular epithelium cadherin 54; cancer; HIV infection; anti-HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
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Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   Arigoni
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/note= "Phosphotyrosine"
                                                       /note= "Phosphotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                   Walchli S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG66403 standard; peptide; 15 AA.
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71.4%;
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YNAYOVD 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 AA;
                                                                                                                     WO2004020466-A1
                           Modified-site
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Query Match
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0;
Oy 1 SNPYSAFQVDIIV 13
Db 3 SVPYTEWELSVII 15
Search completed: November 14, 2004, 13:11:15
Job time: 94.3333 secs

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Gaps

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November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds (without alignments) 66.619 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pubpaa/US07
/cgn2_6/ptodata/1/pubpaa/PCT_N
/cgn2_6/ptodata/1/pubpaa/US06_
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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75
1 SNPYSAFQVDIIVDI 15
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Maximum DB seq length: 15
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dd	Αp	Ap	Appl	dd,	ddy	App	Ap	Ap	Ap	Ap	Ap	ΑÞ
		332, App	37,	7,	30, Aj		•		39,	39,	1019,	20,	1021,	022,
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10		394	748	118	1761	313	313	313	748	118	313	313	313	313
SUMMARIES		35-	 0E	93-1	12-	34-6	34-6	34-6		93-7	34-8	34-8	34-6	34-8
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.4 US-10-084-813-1023	.4 US-10-084-813-1024	.4 US-10-286-457-177	US-10	4 US-10-084-813-780	.4 US-10-084-813-781	.4 US-10-084-813-782	10-084-813-	.4 US-10-084-813-784	.4 US-10-084-813-785	.4 US-10-084-813-786	.4 US-10-084-813-787	.4 US-10-084-813-788	.4 US-10-354-240-95	4. US-10-151-882-26	US-09-927-180-3	.4 US-10-334-726-118	.4 US-10-334-726-220	.6 US-10-408-765A-3056	US-10		.5 US-10-403-847-83				0	9	.6 US-10-327-598-705	-60-SN	.3 US-10-039-645-70	.4 US-10-139-084-70	.4 US-10-239-313A-238
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## ALIGNMENTS

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                                                                               APPLICANT: FASULO, LISA M.
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
APPLICANT: HOLT, GORDON DUANE
APPLICANT: STIGER, THOMAS R.
TITLE OF INVENTION: BIOWARKERS OF LIVER RESPONSE
FILE REFERENCE: POA-003.01
CURRENT APPLICATION NUMBER: US/10/285,394
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,964
PRIOR FILING DATE: 2001-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-880-748-3097
; Sequence 3097, Application US/09880748
Sequence 332, Application US/10285394; Publication No. US20030228583A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.5%;
                                                                APPLICANT: AMACHER, DAVID E.
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 412
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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LENGTH: 15
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Sequence 30, Application US/09842776A
Publication No. US20040023316A1
General Information:
General Information:
APPLICANT: CONNEX GMBH
TITLE OF INVENTION: IN THE STOCL
THE STOCK
TITLE OF STOCK
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APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT APPLICATION NUMBER: PCT/US00/23505
PRIOR PILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Complementarity determining region (CDR3) of an OTHER INFORMATION: antibody heavy chain directed to a beta-urease OTHER INFORMATION: epitope (alternative sequence)
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Publication No. US20030068615A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1.
4; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                3 SPYDAFDI 10
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6 SNPYS 10
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                                                                                                                          RESULT 4
US-09-842-776A-30
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US-10-084-813-973
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Sequence 3097, Application US/10293418

Publication No. US20030223996A1

GENERAL INPORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5-29-29

CURRENT PELING DATE: 2002-11-27

FRIOR APPLICATION NUMBER: 60/331, 469

PRIOR APPLICATION NUMBER: 60/331, 469

PRIOR APPLICATION NUMBER: 60/331, 469

PRIOR APPLICATION NUMBER: 60/340, 817

PRIOR APPLICATION NUMBER: 60/340, 817

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/277, 379

PRIOR APPLICATION NUMBER: 60/270, 379

PRIOR APPLICATION NUMBER: 60/270, 379

PRIOR APPLICATION NUMBER: 60/270, 319

PRIOR APPLICATION NUMBER: 60/270, 319

PRIOR APPLICATION NUMBER: 60/210, 816

PRIOR PRIING DATE: 2000-06-16

NUMBER: 0F SEQ ID NOS: 3247

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                                                                       APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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Pred. No. 2.5e+02;
2; Mismatches 2
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Publication No. US20030059937A1
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Best Local Similarity 50.0
Matches 4; Conservative
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US-09-880-748-3097
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Best Local Similarity
Matches 4; Conserval
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LENGTH: 10
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FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT PILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/311,469
PRIOR PILING DATE: 2001-11-16
PRIOR PLICATION NUMBER: 60/340,817
PRIOR PLICATION NUMBER: 60/294,48
PRIOR PLICATION NUMBER: 60/293,499
PRIOR PLILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR PLILING DATE: 2001-03-16
PRIOR PLILING DATE: 2001-03-16
PRIOR PLILING DATE: 2000-01-17
PRIOR PLILING DATE: 2000-01-17
PRIOR PLILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR PLILING DATE: 2000-06-16
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      TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 4.1e+02;
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               THIRE COLINGATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 200-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.0
Best Local Similarity 57.1
Matches 4; Conservative
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Matches 4; Conservative
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US-09-880-748-2839
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ORGANISM: Homo sapiens
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Sequence 975, Application US/10084813

Publication No. US20303068615A1

GENERAL INFORMATION:

APPLICANT: SAXINGER. CARL

TITLE OF INVENTION: POLYBEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

FILE REFRENCE: 218075

CURRENT APPLICATION NUMBER: US/10/084,813

CURRENT FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/151,270

PRIOR APPLICATION NUMBER: US 60/151,270

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 975

LENGTH: 9
               Sequence 974, Application US/10084813
Sequence 974, Application US/10084813
Publication No. US20030066615A1
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 216875
CURRENT FILING DATE: 2002-02-27
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PATENTIN VERSION 3.1
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; Sequence 2839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 57.1
Matches 4; Conservative
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2 FKIDIVV 8
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1 FKIDIWV 7
US-10-084-813-974
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LENGTH: 9
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US-10-084-813-1022
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Sequence 1019, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT FILING DATE: 2002-27
; PRIOR PELICATION NUMBER: PC7/US00/23505
; PRIOR APPLICATION NUMBER: PC7/US00/23505
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1019
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Publication No. US20030066615A1

GENERAL INFORMATION:

TITLE OF INVENTION: POLYBEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

FILE REPERENCE: 215875

CURRENT APPLICATION NUMBER: US/10/084,813

CURRENT APPLICATION NUMBER: PC7/US00/23505

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SEQ ID NO 1220

LENGTH: 12
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; Publication No. US20030068615A1
; GENERAL INFORMATION:
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Matches 4; Conservative
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## SEQUENCE 1022, Application US/10084813
| Publication No. US20030068615A1 |
| Publication No. US20030068615A1 |
| GENERAL INFORMATION: |
| APPLICANT: SAXINGER, CARL |
| TITLE OF INVENTION: POLYEPPIDES THAT BIND HIV GP120 AND RELATED NUCLEIC |
| TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE |
| FILE REPERENCE: 218875 |
| CURRENT APPLICATION NUMBER: US/10/084,813 |
| CURRENT FILING DATE: 2002-02-27 |
| PRIOR PRILING DATE: 2000-08-25 |
| PRIOR FILING DATE: 1999-08-27 |
| NUMBER OF SEQ ID NOS: 1242 |
| SEQ ID NO 1022 |
| PRIOR FILING DATE: NUMBER PARENTED NOS: 1242 |
| SEQ ID NO 1022 |
| SED ID NO 1022 |
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| CONTUMENT NUMBER PARENTED NUMBER PARENTE
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APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REPERENCE: 215875
CURRENT PAPLICATION NUMBER: US/10/084,813
CURRENT PAPLICATION NUMBER: US/10/080/23505
PRIOR PAPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PLANCE DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PARENTIN VERBION 3.1
LENGTH: 12
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; Sequence 1023, US20030068615A1
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: AACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REPERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
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US-10-084-813-1022
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Pred. No. 4.6e+02;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Sequence 1024, Application US/10084813
; Sequence 1024, Application US/2003068615A1
; Publication No. US2003068615A1
; GENERAL INFORMATION:
APPLICANT: SAXINGEN: CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLBIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 218875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PALENTIN VERSION 3.1
; SEQ ID NO 1024
; LEMOTH: 12
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                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Artificial Sequence
FATURE: PEATURE:
COTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1023
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CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR PILING DATE: 2000-08-25
PRIOR PELING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SEQ ID NO 1023
LENGTH: 12
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2 FKIDIVV 8
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1 FKIDIWV 7
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US-10-084-813-1024
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/cgm2 6/ptodata/1/iaa/PcTUS COMB.pep:*
/cgm2 6/ptodata/1/iaa/PcTUS COMB.pep:*
           GenCore version 5.1.6
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US-08-933-823-110
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US-09-413-223-110
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US-08-116-33
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                1 SNPYSAFQVDIIVDI
                                                                                                                          US-09-831-253F-4
75
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Match Length
                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 15
                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                       Perfect score:
                                                                                                                                                   Sequence:
                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                     Database
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No
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                                                                               Run on
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Sequence 110, Application US/08934222

Sequence 110, Application US/08934222

Patent No. 5928896

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
CITY: Washington
STATE: D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                 Sequence 99, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 2837, 1
Sequence 2840, 1
Sequence 2840, 1
Sequence 2840, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREADTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
PILING DATE: 19-SEPT-1997
PRILING DATE: 03-MAY-1996
PILING DATE: 03-MAY-1996
PILING DATE: 29-OCT-1993
PRILING DATE: 39-APR-1993
PRILING DATE: 31-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: 18-OCM-1993
REGISTRATION NUMBER: 33.751
REGISTRATION NUMBER: 34.751
US-09-187-859-2837
US-09-839-5428-2837
US-09-839-5428-2840
US-09-839-5428-2840
US-08-621-803-99
US-08-621-803-99
US-08-65-430-39
US-08-65-430-39
US-09-217-352-99
US-09-217-433-10
US-08-712-433A-10
US-08-712-433A-10
US-08-712-433A-10
US-08-712-433A-10
US-08-713-739-10
US-08-718-739-10
US-08-718-739-10
US-08-718-739-10
US-08-718-739-10
US-08-718-738-10
US-08-718-738-10
US-08-718-738-10
US-08-718-738-10
US-08-718-738-10
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amino acid
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Sequence 110, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 14;
                                                                                                             COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US94/04294
FILING DATE: 20-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
FILING DATE: 23-APR-1993
ATTONINY/AGENT INFORMATION:
AMADER TO THE TABLE TO THE TABLE TAB
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/U894/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 2; I
Pred. No. 1.3e+02;
2; Mismatches 1;
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STREET: Suite 500, 3000 K Street NW
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1.
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
      Washington
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                                                                USA
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US-08-532-818-110
                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-207-621-110
; Sequence 110, Application US/09207621
; Sequence 110, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction (
NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: ZUGO,

COMPUTE: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
PILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/532,818
FILING DATE: 09-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISAGEON, JOHN P.
REGISTRATION NUMBER: 33,751
REGISTRATION NUMBER: 33,751
REFERENCE/LOCKET NUMBER: 040433/0148
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    Sequence 110, Application US/08933402
Patent No. 5948887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: 14-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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Matches 4; Conserv
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1 NPWTVFO 7
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NPYSAFO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-933-402-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Sequence 110, Application US/08934224

Sequence 110, Application US/08934224

Barent No. 6100044

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

ADDRESSEE: Foley & Lardner
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.0%; Score 27; DB 3; Length 14; 57.1%; Pred. No. 1.3e+02; ive 2; Mismatches 1; Indels
                                        IndelB
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ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
            Pred. No. 1.3e+02;
                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTLING DATE:
PRIOR DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: IBacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite 500, 3000 K Street NW CITY: Washington
               57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
3Y: linear
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      Best Local Similarity
Matches 4; Conserv
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NPWTVFQ 7
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1 NPWTVFQ 7
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US-08-933-843-110
                                                                                                                                                                                                                                                RESULT 6
US-08-934-224-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Sequence 110, Application US/09231797

Patent No. 6084066

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-

TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 2; I
Pred. No. 1.3e+02;
2; Mismatches 1;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03.AMX-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21.APR-1994
PRIOR APPLICATION DATA:
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
FILING DATE: 29-0CT-1993
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~WEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%;
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3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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1 NPWTVFQ 7
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GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Oblypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES:
ADDRESSEE: FOLEY & Lardner
STREET: Suite 500, 3000 K Street NW
COLLY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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CORRATING SIGTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: 06/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27; DB 3; 1
Pred. No. 1.3e+02;
2; Mismatches 1;
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
FILING DATE: 03-MAY-1996
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 23-CT-1993
ATTONNEY/AGENT INFORMATION:
NAME: 18aceon, John P.
REGISTRATION NUMBER: 33,751
REFERENCY/OCKET NUMBER: 33,751
REFERENCY/OCKET NUMBER: 33,751
REFERENCY/OCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 110, Application US/09413492 Patent No. 6258550
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 4; Conserv
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1 NPWTVFO 7
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USA
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COUNTRY: US
ZIP: 20007
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US-09-413-492-110
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Sequence 110, Application US/08934223
Sequence 110, Application US/08934223
Sequence 110, Application US/08934223
Sequence 110, Application US/08934223
Sequence 110, Application Sequence Tritle OF INVENTION: Polypeptides That Include Conformation-TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction TITLE OF INVENTION: Site NUMBER OF SEQUENCES: 153
CORRESPONDENCES: 153
CORRESPONDENCES: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
Constraining Groups Which Flank A Protein-Protein Interaction Site 153
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                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC COMPALIBLE
COMPUTER: IN PC COMPALIBLE
COMPUTER: IN PC COMPALIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
SUGTWARE: Patentin Release #1.0, Version #1.25
PLING DATE: 19-SEPT-1997
PRIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: 0.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
ATPONDEY/AGBAT INPOMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATPONDEY/AGBAT INPOMBATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPACIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILIGATION NUMBER: US/08/934,223
FILIGATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
     TITLE OF INVENTION: Constraining Group
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardher
STREET: Suite 500, 3000 K Street NW
CITY: Washington
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LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 57.1
Matches 4; Conservative
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1 NPWTVFO 7
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APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER: READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/422,106
FILING DATE: 14-APR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-ULL-1994
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TOWNSTORM: 7 amino acids
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APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.7%; Score 26; DB 1; Length 7; 57.1%; Pred. No. 3.8e+05;
                                                                                                                                                                                                  34.7%; Score 26; DB 1; Length 7; 57.1%; Pred. No. 3.8e+05;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,716
FILING DATE: 23-OCT-1996
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                                                                                                                                                                                                                                                            2; Mismatches
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NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                              single
                                                      linear
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NPYSAFQ 8
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1 NPHSGFR 7
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1 NPHSGFR 7
                                                TOPOLOGY: link
MOLECULE TYPE: |
HYPOTHETICAL: N
                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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US-08-422-106-3
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US-08-281-193-3
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Patent No. 5466595
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%; Score 27; DB 4; Length 15; 45.5%; Pred. No. 1.4e+02; tive 3; Mismatches 3; Indels
                                                                                                                                                                    Length 14;
                                                                                                                                                                                                                                1; Indels
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CCATION: (1)..(15)
COTHER INFORMATION: Cryj2 peptide, Figure 2, Row 12
US-09-142-254D-95
                                                                                                                                                                    Score 27; DB 3; I
Pred. No. 1.3e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95, Application US/09142524D
Patent No. 6719976
GENERAL INFORMATION:
APPLICANT: Sone, Toshio
APPLICANT: Kume, Akinori
APPLICANT: Iwama, Akiko
APPLICANT: Iwama, Akiko
APPLICANT: Kino, Kohsuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/281,193
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                          36.0%;
57.1%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                           LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                    Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.0
Best Local Similarity 45.5
Matches 5; Conservative
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                          2 NPYSAFQ 8
                                                                                                                                                                                                                                                                                                                        1 | | :: | |
1 NPWTVFQ 7
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                                                                                                             US-09-413-492-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-142-524D-95
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US-08-281-193-3
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LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3. Application US/0855568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Tang, Jim
APPLICANT: Calcium Independent Phospholipase A2/B
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS: 35
CORPERS MADDRESS: 35
CONTYR: U.S.A.
ZIP: 02140
COMPUTER: READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tan PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/555,568B
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Pred. No. 3.8e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                Score 26; DB 2; Length 7; Pred. No. 3.8e+05; 2; Mismatches 1; Indels
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown. Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 498-8224
TELEFAX: (617) 476-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                              7 amino acids
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                                                                                                                                                                        single
                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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1 NPHSGFR 7
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NPHSGFR 7

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                                                                               GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COMPUTRY: U.S.A.
ZIP: 02140
COMPUTRY: ISP PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRYT APPLICATION NUMBER: US/09/519,223
FILLING DATE:
APPLICATION NUMBER: US/09/519,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
RESULT 15
18-09-519-223-3
Sequence 3, Application US/09519223
Patent No. 6274140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scote A:
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 896-824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 7 amino acids
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STRANDEDNESS: sir
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Matches 4; Conserv
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1 NPHSGFR
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RESULT 3
PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
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neuromodulatory pe
seminal vesicle pr
D-SP2.5 region - m
T-cell receptor ga
pullulanase (EC 3.
glycine reductase
T-cell receptor be
hypothetical prote
acylase - Kluyvera
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gene c-mpl protein
Ig heavy chain CRD
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platelet-deriedge
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hypothetical prote
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T-cell receptor be
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hypothetical pepti
cell aurface adhes
hypothetical prote
T-cell receptor be
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Vesicle associated
leucokinin VI - Ma
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                                                                                              November 14, 2004, 13:57:40 ; Search time 37 Seconds (without alignments) 23.404 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                   791
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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                                                                 - protein search, using sw model
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PN0649
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PT0661
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Maximum Match 100%
Listing first 45 su
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48
1 TSLMIWTWM 9
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
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                                                                 OM protein
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No.
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acetylcholinestera litorin 2-Glu - Au litorin 1 - Austra caldesmon - rabbit xenopsin-related p xenopsin-related p bradykinin-potenti RPCH-related neuro T-cell receptor be cholecystokinin-5 hypothetical prote neuropeptide - sea gut pentapeptide - ig heavy chain CRD T-cell receptor be receptor be cholecystokinin-5 hypothetical prote neuropeptide - sea gut pentapeptide - ig T-cell receptor be T-cell receptor be	transferase (EC 2.4.1.17), hepatic - rat (fragment) names: UDP-glucuronyltransferase attus norveglucus (Norway rat) ul-1992 #text_change 07-Feb-1997 PX0008 PX0008 ification and properties of a form of UDP-glucuronyltransferase from liver mi number: PX0008; MUD:89197852; PMID:3149280 number: PX0008; MUD:89197852; PMID:3149280 px0008 ype: protein 1-7 <yok> spe: protein 1-7 <yok> spilarity 50.0%; pred: No. 2.88+05; Similarity 50.0%; pred: No. 2.88+05; 1 TSIMIW 6     ISIMIW 6     ISIMIW 6     ISIMIW 6     ISIMIW 6</yok></yok>	RESULT 2 S09652 Supportetical protein (aacC2 3' region) - Enterobacter cloacae (fragment) C;Species: Enterobacter cloacae C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999 C;Accession: S09652 Rylisgenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M. Antimicrob. Agents Chemother. 33, 1153-1159, 1989 A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant invol A;Reference number: S09651; MUID:90024972; PMID:2552900 A;Reference source number: A;Reference source determinant invol A;Reference source number: S09651, MUID:90024972; PMID:2552900 A;Residues: 1-7 <vli>A;Residues: 1-7 <vli>A;Cross-references: EMBL:X51534; NID:940878; PIDN:CAA35914.1; PID:9581034</vli></vli>
A41117 S07205 S07205 A07204 JS0302 JS0302 P37196 A34626 A34626 A34626 A10954 A60803 A60803 P10253 P10259 P10259	RESULT 1  PX0008  Glucuronosyltransferase (EC 2.4.1.17), hepat NiAlternate names: UDP-Glucuronyltransferase C;Species: Rattus norvegicus (Norway rat) C;Accession: PX0008 R;YOKOTA, H.; Yuasa, A.; Sato, R. R;YOKOTA, H.; Yuasa, A.; Sato, R. R;YOKOTA, H.; Yuasa, A.; Sato, R. A;Title: Purification and properties of a fo A;Reference number: PX0008; MUID:89197852; PA;Accession: PX0008 A;Accession: PX0008 A;Ccession: PX0008 A;Cce	(aacC2 3' region) - E ter cloacae #sequence_revision 12-; ; Ketelaar-van Gaalen, hemother. 33, 1153-115 sequence of the aacC2 \$09651; MUID:90024972; ************************************
000000000000000000000000000000000000000	14.1 Only 2 (Nor Nor R. R. J. D. J. D. J. Be;	" re _rev 33, of t UID:
<b>ᢁᠳᠳᠳᠳᢋᢋ</b> ᠩᡢᡢᠬᠬᠬᠬ	ferase (EC 2.4.] : UDP-glucurony) 22 #sequence_reny 88, A.; Sato, R. 531-536, 1988 tion and propert r: PX0008; MUID protein YOK> syltransferase; 1arity 50.0%; Conservative MIW 6 ::	(aacc2 3' region) ter cloacae the cloacae #sequence_revision ; Ketelaar-van Gaal hemother. 33, 1153. sequence of the aac S09651; MUID:90024 }
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	ansfer mess U rus no rus XX008 YX008 YX008 icatio mber: XY0K YCOSYI imilar imilar COn imilar	rotei - 1995 - 1995 09652 0 J.E ents otide mber: 09652 09652
	RESULT 1  PX0008  glucuronosyltransferase (EC 2.4.1.17) N;Alternate names: UDP-glucuronyltrar C;Saccies: Rattus norveglous (Norway C;Date: 17-Jul.1992 #sequence_revisic C;Accession: PX0008 R;YOKOta, H.; Yusas, A.; Sato, R. R;YOKOta, H.; Yusas, A.; Sato, R. R;YOKOta, H.; Yusas, A.; Sato, R. A;Title: Purification and properties A;Reference number: PX0008; MUD:8918 A;Accession: PX0008 A;Accession: PX0008 A;Accession: PX0008 C;Keywords: glycosyltransferase; hexc Cuery Match Best Local Similarity 50.0%; Pre Matches 3; Conservative 2; Ob 1 TSLLWW Bb 1 TKLLWW Bb 1 TKLLWW Bb 1 TKLLWW Bb 2 TKLLWW B 2 TKLLWW B 2 TKLLWW B 3 TKLLWW B 3 TKLLWW B 3 TKLLWW B 3 TKLLWW	RESULT 2 S09652 hypothetical protein (aacC2 3' region) C;Species: Enterobacter cloacae C;Date: 12-Feb-193 #sequence_revision C;Accession: 806652 R;Vilegenthart, J.S.; Ketelaar-van Gaa Antimicrob. Agents Chemother. 33, 1153 A;Title: Nucleotide sequence of the aa A;Reference number: 809651, MUID:90024 A;Accession: 809652 A;Molecule type: DNA A;Residues: 1-7 <vli>A;Cross-references: EMBL:X51534; NID:9</vli>
	RESULT 1 PX0008 glucuronosyl N.Alternate C,Species: 17-C;Accession: C,Accession: C,Accession: A,Title: Pur A,Reference A,Residues: C,Keywords: C,Keywords: C,Keywords: Ouery Matches Apthony	RESULT S09652 Nypoth C; Spec C; Acce R; Vile Antimil A; Refe A; Refe A; Acce A; Resi A; Resi
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Gaps

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0; Indels

Score 18; DB 2; Length 7; Pred. No. 2.8e+05; 2; Mismatches 0; Indels

h 37.5%; Similarity 50.0%; 2; Conservative

Query Match Best Local Similarity Matches 2; Conserv

3 LMIW

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hypothetical peptide PAII promoter region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GDB:120297, OMIM:173360
A, Map position: 7q21.3-7q22
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1es 2; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 0.2-Unn-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1602
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
B;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Title: Mode: 178, 317-329, 1993
A;Title: Mode: Use the characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: B34835
R;Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A;Reference number: A34835; MUID:90160310; PMID:2106132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0661
R;Feeney, A.J.
T;Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C,Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
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A;Renidues: 1-6 <YEE>
A;Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C;Keywords: DNA binding
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Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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A;Residues: 1-4 <FEE>
A;Cross-references: UNIPROT:08BZQ7; UNIPROT:08CCN5
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor
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40.0%; Pred. No. 2.8e+05;
tive 2; Mismatches 1;
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Best Local Similarity 66.7%;
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity 40.0
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: B34835
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Chacesion: 155302
Ribawson, S. J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 268, 10739-10745, 1993
J. Biol. Chem. 268, 10739-10745, 1993
J. Riol. Chem. 268, 10739-10745, 1993
J. Reference number: 155382
J. Riol. Signature: 175882
J. Riol. Signature: 175882
J. Riol. Signature: 175882
J. Riol. Signature: 175882
J. Comment: This is the hypothetical translation of a sequence from the PAII gene promotes
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Cipate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

Cipate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

Cipate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #s.; Glasner, J.D.; Rose, D.J.; Mayhew,,

Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A88480; MUID:21074935; PMID:11206551

A;Accession: G88502

A;Actures: preliminary

A;Molecule type: DNA

A;Residues: 1-9 <STO>
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A;Residues: 1-9 <LIA>
A;Cross-references: UNIPROT:09R5M1
A;Note: sequence extracted from NCBI backbone (NCBIP:85442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%; Score 16; DB 4; Le
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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D-SP2.5 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
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                                                                                                                                                                             h 31.2%;
Similarity 25.0%;
1; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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A;Molecule type: protein
A;Residues: 1-7 <MIN>
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Best Local Similarity
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A; Residues: 1-9 < RES>
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4 MSVW 7
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A;Cross-references: UNIPROT;Q8X4G1; GB:AE005174; NID:g12515957; PIDN:AAG56883.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Gene:ics:
A;Gene: Z2947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: S33244
R,Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
R,Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A,Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of A,Reference number: S33244; MUID:93265912; PMID:8495720
                                                                                                                                                                                                                                                                                                                                                                                                          R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor
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C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33245
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
                                                                                                                                                                                                                                                                                                                                                   T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C;Accession: PT0586; PT0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuromodulatory peptide WWamide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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                                                                                                             Score 16; DB 2; Length 9;
Pred. No. 2.8e+05;
1; Mismatches 2; Indels
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100.0%; Pred. No. 2.8e+05;
vative 0; Mismatches 0;
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                                                                                                               33.3%;
50.0%;
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Best Local Similarity 100...
Lac 2; Conservative
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A;Molecule type: protein
A;Residues: 1-7 <MIN>
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Best Local Similarity
Matches 3; Conserv
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1 MTYTFM 6
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A; Residues: 1-7 <FEE>
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MSVW 7
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DNA 2, 105-111, 1983
A,Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites
A,Reference number: IS2974; MUID:83261204; PMID:6307619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Special Achatina fulica (giant African snail)
C.Special Achatina fulica (giant African snail)
C.Special 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C.Accession: S33246
R.Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A.Fitle: Wamidel-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the A.Reference number: S33244; MUID:93265912; PMID:8495720
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33245
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>
A;Cross-references: UNIPROT:P35919
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seminal vesicle protein IV - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.2%; Score 15; DB 2; Length 7; Best Local Similarity 25.0%; Pred. No. 2.8e+05; Matches 1; Conservative 2; Mismatches 1; Indels
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Pred. No. 2.8e+05;
2; Mismatches 1;
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 741946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
C;Keywords: T-cell receptor

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Gaps

0;

Score 14; DB 2; Length 6; Pred. No. 2.8e+05; 1; Mismatches 0; Indels

29.2%;

Query Match
Best Local Similarity 50.0
Matches 1; Conservative

Search completed: November 14, 2004, 14:07:59 Job time: 49 secs

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11, Appl 3, Appli 3, Appli 3, Appli 3, Appli 3, Appli 18, Appli 18, Appli 56843 Appl

Sequence 3 Sequence 1 Sequence 1 Sequence 5

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Sequence 173, Application US/09177249
; Sequence 173, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Goad, Nir
; APPLICANT: Margossian, Linda
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION NUMBER: US/09/177, 249
; CURRENT FILING DATE: 1998-10-22
; EARLIER RELING DATE: 1998-10-22
; EARLIER PILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: IT
PCT-US93-03076-11
US-08-281-193-3
US-08-422-106-3
US-08-735-716-3
US-09-515-56B-3
US-09-512-3-3
US-09-527-1180-3
US-09-27-1180-3
US-09-327-1180-3
US-09-327-1180-3
US-09-327-1280-3
US-09-444-818-304
US-08-444-818-305
US-08-819-286-22
US-08-819-286-22
US-08-819-286-23
US-08-819-286-23
US-08-819-286-23
US-08-819-286-23
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US-08-819-286-24
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Sequence 5, Application US/08116733

PATONIC NO. 5516632

APPLICANT: PALKER, Thomas J.

APPLICANT: HAYNES, Barton F.

TITLE OF INVENTION: SYNTHETIC PEPTIDES

NUMBER OF SEQUENCES. 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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ORGANISM: Arabidopsis sp
     Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-177-249-173
   RESULT 2
     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Appl Sequence 21, Appl Sequence 11, Appl Sequence 110, Appl Sequence 110, App  Sequence 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 173, App
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds (without alignments) 84.242 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
                       5.1.6
Compugen Ltd.
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US-08-116-733-5
US-08-1819-286-20
US-08-819-286-21
US-08-630-052-25
US-08-630-052-25
US-08-934-222-110
US-08-934-222-110
US-08-934-224-110
US-09-231-797-110
US-09-231-843-110
US-09-231-244-110
US-08-934-224-110
US-08-934-245-110
US-08-934-245-110
US-08-934-245-110
US-08-934-245-110
US-08-935-925C-8
US-08-935-925C-8
US-08-935-925C-8
US-08-935-925C-8
US-08-935-925C-9
US-08-935-925C-9
US-08-127-4994-18
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       478139 segs, 66318000 residues
                     GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                      US-09-831-253F-4
75
1 SNPYSAFQVDIIVDI 15
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                                                                                                                                                                                                                                                                                                                                                                                                              seg length: 0
seg length: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                              OM protein
                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                 Run on:
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Gaps

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Length 17; Indels

Gaps

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1; Indels

DB 3; Length 16; 66;

us-09-831-253f-4.rai

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1; Mismatches
                                                           not relevant
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                                                                                                                                                               38.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                   LENGTH: 16 amino acide
TYPE: amino acid
STRANDEDNESS: not relev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acide
                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: peptide
US-08-819-286-21
                                                                                                                                                                                                                                                                     3 OVDEVVDI 10
                                                                                                                                                                                                                                                8 QVDIIVDI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVDIIVDI 15
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                                                                            linear
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Patent No. 6169074
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 22;
Pred. No. 27;
2; Mismatches 3; Indels
            COUNTRY: U.S.A.

ZIP: 22201-4714

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,733
FILING DATE: 07-SEP-1993
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, WARY J.
REFIERBUCE/ODCKET NUMBER: 1579-33
TELECOMMUNICATION NUMBER: 1579-33
TELECOMMUNICATION INFORMATION:
TELEBRAX: (703) 816-4100
TELEBRAX: (703) 816-4100
TELEBRAX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LEMGTH: 22 aming acids
LEMGTH: 22 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34,842
.ee. 07349/005001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIASSIPTICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 075
TELECOMMUNICATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-116-733-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SNPYSAFOVDI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSPYWKFOHDV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-819-286-20
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Sequence 21, Application US/08819286

Patent No. 6169074

GENERAL INFORMATION:

APPLICANT: MOUTAID,

TITLE OF INVENTION: PEPTIDE INHIBITORS OF

TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                      COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFTANTON: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB
Pred. No. 86;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-08-630-052-25
; Sequence 25, Application US/08630052
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STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NPYSAFQVDIIVD 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-652-877-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19426-0107
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-476-515A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                 COUNTRY:
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                                 APPLICANT: Brent, Roger
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29; DB 3; Length 20;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                         SIGNATE: MASSACHMENTES
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,052
FILING DATE:
CLASSIFICATION TOWNER: 08/504,538
FILING DATE: JULY 20, 1995
APPLICATION NUMBER: 08/504,538
FILING DATE: JULY 20, 1995
ATTORNEY/AGENT INFORMATION:
NAME: KATEN F. LECH
REGISTRATION NUMBER: 007086/311001
TELECOMMUNICATION NUMBER: 007086/311001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                               E: Fish & Richardson, P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Crumley, Gregg R.
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Morse, Clarence C.
APPLICANT: Morse, Clarence C.
APPLICANT: Hjalm, Goran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.7%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
                                                                                                                                                                                                                                 STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-630-052-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PYSAFQVD 10
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Gaps
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Fatent No. 6239270
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Crumley, Greeg R.
APPLICANT: Crumley, Greeg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Mirray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Martin Savitzky
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,
STREET: 3C43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27.5; DB 3;
Pred. No. 1.3e+02;
1; Mismatches 2;
                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: SAV12AXY, MARTÍN
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 39,699
REFERENCE/DOCKET NUMBER: 3155E-US
TELECOMMUTICATION INFORMATION:
TELEPHONE: 610-454-3808
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FENTANTH: 17 amino acids
ZIP: 19426-0107
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
```

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GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 33-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISBACSON, JOHN P.
REGISTRATION NUMBER: 33-751
REGISTRATION NUMBER: 33-751
REGISTRATION NUMBER: 33-751
                                                                                                                                                                                                                                                                                                                                                                                                  36.0%; Score 27; DB 2; 1
57.1%; Pred. No. 1.3e+02;
iive 2; Mismatches 1.
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Pred. No. 1.3e+02;
FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 3,751
REGISTRATION NUMBER: 040433/0148
FREFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-933-402-110
; Sequence 110, Application US/08933402
; Patent No. 5948887
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INFORMATION FOR SEQ ID NO: 110:
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57.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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ADDRESSEE: Foley & La
                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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NPWTVFQ 7
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TOPOLOGY:
US-08-934-222-110
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Patent No. 5928896

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
36.7%; Score 27.5; DB 3;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2;
                 MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NUMBE: SAVILEYY, MATTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner STREET: Suite 500, 3000 K Street NW CITY: Washington STATE: DC STATE: USA ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A135E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NPYSAFQVDIIVD 14
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
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Sequence 110, Application US/09231797

Patent No. 6084066

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
CITY: Washington
STREET: D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                               COFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20007
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04
INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 14 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 57.1
Matches 4; Conservative
  NUMBER OF SEQUENCES:
                                                                                    Washington
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1 NPWTVFQ 7
                                                                                                                           USA
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                                                                                                                           COUNTRY: U
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TOPOLOGY:
US-08-532-818-110
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                                                                                 CITY: 1
STATE:
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Constraining Groups Which Flank A Protein-Protein Interaction
Site
                                                                                                                                                                                   Sequence 110, Application US/09207621

Patent No. 5952465

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction (
NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:
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  Indels
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APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRINCATION NUMBER: US/09/207,621
FILING DATE:
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: 08/532,818
FILING DATE: 13-MAY-1994
PRIOR APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 23-APR-1993
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 23-APR-1993
APPLICATION NUMBER: US. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides Tha
TITLE OF INVENTION: Constraining Gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
5
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04(
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DOX
CHRDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1-
4; Conservative
                                       2 NPYSAFQ 8
                                                             ||:: ||
1 NPWTVFQ 7
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1 NPWTVFQ 7
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US-08-532-818-110
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Matches
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                                                           Length 14;
                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentln Pel-BoS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION NUMBER: US.08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING BATE: 23-OCT-1993
RIOR APPLICATION NUMBER: US. 08/051,741
FILING BATE: 23-APR-1993
ATTONINTY/AGRIT INFORMATION:
ANAMER: 23-APR-1993
ATTONINTY/AGRIT INFORMATION:
                                                           Score 27; DB 3;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-934-223-110
Sequence 110, Application US/08934223
Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
                                                           36.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 amino acids
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                                                                                                    Conservative
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                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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1 NPWTVFQ 7
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                                                                                                                                               2 NPYSAFQ
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COUNTRY: US
ZIP: 20007
          US-08-934-224-110
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US-08-934-224-110
Sequence 110, Application US/08934224
Sequence 110, Application US/08934224
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
APPLICANT: STITLE OF INVENTION: Stie
AUTHER OF INVENTION: Stie
ADDRESSEE: Foley & Lardner
ADDRESSEE: Foley & Lardner
ADDRESSEE: Stite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE: 03-MS-1996
APPLICATION NUMBER: 08/532,818
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: CT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 23-APR-1993
APPLICATION NUMBER: US. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                   NAME: Isacson, John P.
RECISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TYPE: amino acid
US-09-231-797-110
              FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION WIMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: 18acson, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Isacson, John P.
REGISTATION NUMBER: 33,751
REFERRICE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                         36.0%;
57.1%;
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LENGTH: 14 amino acids
TYPE: amino acid
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ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
APPLICATION NUMBER:
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STATE: DC
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1 NPWTVFQ 7
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Manjunatha
Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction
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APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A
TITLE OF INVENTION: Constraining Groups Which Flank A
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSED: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
GITY: Washington
STRATE: DC
COUNTY: USA
ATTATE: DC
COUNTY: USA
COUNTY: USA
ATTATE: DC
COUNTY: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CORREATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CORREATING DATE:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/051,741
FILING DATE: 23-APPL
APPLICATION NUMBER: 33,751
REFERENCE CHARATING ACIA
SEQUENCE CHARATING ACIA
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARATERISTICS:
LEBOTH: HA mainto acids
TYPE: aminto acids
TYPE: aminto acids
TYPE: aminto acids
TYPE: TILING ACIDS
TOOLOGY: TILING ACIDS
TYPE: TILING
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Best Local Similarity 57.1
Matches 4; Conservative
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US-08-934-223-110
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Search completed: November 14, 2004, 12:08:47 Job time: 11.8085 secs

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Gaps ö

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November 14, 2004, 11:57:25; Search time 43.4043 Seconds (without alignments) 123.973 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                            OM protein - protein search, using sw model
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75
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Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 SNPYSAFQVDIIVDI 15 Scoring table: Sequence: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_23Sep04:\* 1: geneseqp1980s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\*geneseqp2001s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ption		48 Transtorm	66 Transform	51 Transform	99 Transform	59 Transform		37 Anti-Stap		28 HTLV-I gp	25 Synthetic				PTP1B	05 PTP1B pho	PTP1B		PTP1B	82 N-termina .	51 P. papata	<u>а</u>	50 Termitomy	37 Human col	80 P. papata	Hum
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	ΩI		AAY92948	AAY93066	AAY92951	AAY93099	AAY93059	AAY93067	AAW94737	ADL35119	AAR34228	AAY17925	ABP55430	ABR75594	ADN07473	ADL70819	ADL70905	ADL70907	ADL70906	ADL70908	AAR31182	ABR91851	ABR91858	ADC60750	AAG76637	ABR91880	AAG66403
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ф	Query Match		100.0	100.0	86.7	86.7	70.7	62.7	42.7	42.7	42.7	42.7	41.3	41.3	41.3	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	40.0	38.7
	Score		75	75		65	53	47	32	32	32	32	31	31	31	30	30	30	30	30	30	30	30	30	30	30	29
	Result No.	1	_	7	e	4	S	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Aaw43315 Human cal Aab89867 HIV gp120
AAW32131 ABW74026 AAW320254 AAW72723 AAW60111 ABG42547 AAB6040 AAB40012 AAB40012 AAB6092 AAB6092 AAB6092 AAB6092 AAB6093 AAB6092 AAB6093 AAB6093 AAB6093	AAW43315 AAB89867
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## ALIGNMENTS

RESULT 1

AAY92948

Transforming growth factor inhibitory peptide #4. AAY92948 standard; peptide; 15 AA. (first entry) 08-NOV-2000 AAY92948; 

Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.

WO200031135-A1. Homo sapiens. 02-JUN-2000,

98ES-00002465. 99WO-ES000375. 23-NOV-1999; 24-NOV-1998; (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Claim 5; Page 81; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

us-09-831-253f-4.rag

Query Match Best Loc Matches

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AAY93066

RESULT 2 AAY93066

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93131 represent competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                  Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming growth factor inhibitory peptide P145.
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Pred. No. 2.8e-
1; Mismatches
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                   AAY92951 standard; peptide; 14
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85.7%;
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Best Local Similarity 85.7
Matches 12, Conservative
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                                                        AAY92951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Pred. No. 3.9e-07;
; Mismatches 0; Indels
                                                        Length 15;
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                                                 100.0%; Score 75; DB 3; I
1larity 100.0%; Pred. No. 3.9e-07;
Conservative 0; Mismatches 0:
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Matches 15; Conservative (
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                                                                         Local Similarity
les 15; Conserv
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Query Match

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RESULT 3

Length 14; 1; Indels

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors Peptides AAY92945-Y9133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                            Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                   70.7%; Score 53; DB 3; Length 15; 100.0%; Pred. No. 0.0057; ive 0; Mismatches 0; Indels
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                                                                                                                                Disclosure; Page 28; 86pp; Spanish
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                                                                                                                                                                                                                                                                                                                   expression systems) encoding the disease, specifically cirrhosis
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAV92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                  Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                              Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 3; Length 14;
Pred. No. 2.8e-05;
.; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor inhibitory peptide P105.
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                                                                                                                                                                 (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA
                                                                                                                                                                                                                                                                                                                   sequences of the factor or its receptors
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 31; 86pp; Spanish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93059 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, specifically cirrhosis
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85.78;
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                                                                                               99WO-ES000375
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les 12; Conserv
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                                WO200031135-A1.
Homo sapiens.
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those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimecopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; MAb 96-110.
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    .19
/note= "complementarity determining region (CDR)"

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                                                                                                                                                                                             DB 3; Length 15; 0.078; hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-Staph (HAY) 96-110 heavy chain variable region.
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                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                           62.7%; Score 47; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21; Fig 12; 150pp; English.
                                                                                                                          disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                     AAW94737 standard; protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0049871P
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                                                                                                                                                                                                          Local Similarity
hes 10, Conserv
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                                                                                                                                                             Sequence 15 AA;
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Matches
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This invention relates to a novel method for producing a humanised
antibody variable (V) domain or its fragment by optimising sequence
similarity between individual antibody framework regions (FRB) in order
to identify suitable human FRB (hrFB). Specifically, it refers to novel
immune system molecules i.e. humanised monoclonal antibodies that exhibit
custable binding affilinty with reduced immunogenicity in humans. The
present invention describes a method of mutagenising DNA of non-human FRB
concode humanised FRB having an amino acid sequence that is
to encode humanised FRB having an amino acid sequence that is
concode humanised Ight or the selected human FR previously identified
through sequence similarity searching. As such, this method provides
concoder to treat and/or diagnose diseases in humans and animals
concoders to treat and/or diagnose diseases in humans and animals
concoders to treat and/or diagnose diseases in humans and animals
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concoders to treat and/or diagnose diseases
con be generated and provides a rational basis for assembling nearly all
concoders to the method expands the mumber of bettier diagnosic
concoders.

Concoders to treat and/or diagnose diseases
concoders to treat
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of gram positive bacterial infections. Sequences AAW94735-39 represent
heavy chain variable regions of the anti-lipoteichoic antibody 96-100
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; variable domain; framework region; FR; huFR;
immune system molecule; lipoteichoic acid; LTA; Al10; mouse; murine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDR2 of murine anti-LTA (Al10) heavy chain antibody SegID 125.
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ed. No. 72;
Mismatches
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72;
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                                                                                                                     Score 32;
Pred. No.
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Pred. No.
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                                                                                                                                                                    6; Conservative
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                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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                                                                       Sequence 19 AA;
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HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.
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    80 X X C C C C C C C C X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrophilic peptide; antigen determinant; envelope sugar protein; HTLV-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gp46 external envelope glycoprotein. When covalently linked to a carrier monl. the hydrophilic peptide can induce in a mammal the prodn. of high titres of antibodies to gp46 envelope glycoprotein from HTLV-I or -II. The peptide and carrier may be used in vaccines against HTLV-I or -II infection. The peptide may be used in a diagnostic assay to detect the presence and titre of anti-HTLV antibodies. See also AAR34225-57. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                        Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
  Indels
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                                                                                                                                                                                                                                                                                                                   HTLV-I gp46 external envelope glycoprotein fragment 4.
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
                                                                                                                                                                           AAR34228 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17925 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 11; 50pp; English.
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54.5%;
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                                                                            SNNYATEYADSVKD 19
                                       SNPYSAFQVDIIVD 14
                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-1999 (first entry)
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNPYSAFQVDI 11
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SSPYWKFQHDV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palker IJ, Haynes BF;
                                                                                                                                                                                                                                                                                                                                                                               diagnosis; antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-134125/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-1992;
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04-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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Matches
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934) that correspond to at least one of antigen determinants of envelope sugar proteins of HTLV-I and HTLV-I identified in the B lymphatic corpuscle. When bonded covalently to a carrier molecule, the peptides can induce the production of an antibody having a high titre to the gp46 and gp63 envelope sugar proteins of HTLV-I and HTLV-II in mammals. The carrier molecule is preferably a terams toxoid and selected from the group of sequences shown in AAY13935-39. The carrier molecule is preferably bonded to the peptide through at least one spacer molecule (preferably a dipeptide glycine-glycine). The peptides form effectively immunological response to factors causing virus HTLV-I and HTLV-II. The method also provides an effective conjugate having the peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to new synthetic hydrophilic peptides (AAY17922-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic hydrophilic peptide - comprises 25 unit aminoacid that corresponds to at least one antigen determinant of envelope sugar protein(s) of HTLV-I and HTLV-II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.7%; Score 32; DB 2; Length 22;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP55430 standard; peptide; 15 AA.
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Synthetic.
Human lymphotropic virus type
                                                                                                                                                                                                                                              89JP-00029551.
                                                                                                                                                                                                                                                                                                           88US-00153420.
89US-00303436.
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SSPYWKFQHDV
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involves

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drug or therapy administered to a subject,
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es 5; Conservative
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HERATH H M A C.
HOLT G D.
STIGER T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amacher DE, Fasulo LM,
                                                                                                                                                                                                                                         4 YSAFQVDIIVD 14
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                                                                                                                                                                                                                                                              2 YPGSQLDILID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-430566/40
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                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subject sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                            ADN07473;
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                                                                                                                                                                                                                 Matches
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                                          A novel human breast susceptible gene coded protein 10.45 polypeptide, and the polynucleotide encoding it, useful for treating several diseases e.g. embryotic development deformity and tumors.
                                                                                                            The present invention describes human breast susceptible gene coded protein 10.45 (I). Also described is a process for preparing (I) using DNA recombination techniques. (I) can be used for treating several diseases e.g. embryotic development deformity and tumours. The present sequence represents the N-terminal peptide of (I), which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                               Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:332.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomarker; liver response; liver response-associated protein isoform; LRPI; liver response-associated feature; LRF.
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                  DB 5; Length 15;
                                                                                                                                                                                                                                         2; Indels
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                                                                                        Example 5; Page 20 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                             . 84;
                                                                                                                                                                                                                  Score 31;
Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OXFORD GLYCOSCIENCES UK LID.
                                                                                                                                                                                                                                                                                                                                           ABR75594 standard; peptide; 15 AA.
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                                                                                                                                                                                                                  41.3%;
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                                                                                                                                                                                                                                         5; Conservative
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                                                                                                                                                                                                                                                             2 NPYSAFQVDII 12
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                                                                                                                                                                                                                                                                            SPYFKFRUNVI
                      WPI; 2002-529778/57.
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                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                            Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                  Query Match
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Mao Y,
                                                                                                                                                                                                                                                                                                                     RESULT 12
ABR75594
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contacting at least one oligonucleotide probe comprising 10 or more consecutive nucleotides complementary to a nucleotide sequence encoding an LPRI with RNA obtained from a biological sample from the subject or with cDNA copied from the RNA, where the contacting occurs under conditions that permit hybridisation of the probe to the nucleotide sequence if present, detecting hybridisation, if any, between the probe and the nucleotide sequence, and comparing the hybridisation, if any, detected in the above step, with the hybridisation detected in a control sample, or with a previously determined reference range. MI is useful for screening or diagnosing a liver response in a subject, determining the stage or severity of a liver response in a subject, identifying a subject therapy administered to a subject having liver response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of screening (M1) or diagnosing a liver response in a subject, determining the stage or severity of a liver response in a subject, identifying a subject at risk of developing liver response, or monitoring the effect of therapy administered to a subject having liver response. The method involves detecting Liver Response Associated Protein Isoforms (LRPIS) in a test biological sample from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver response; liver response-associated protein isoform; LRPI; drug monitoring; therapy monitoring; liver response-associated feature;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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diseases.

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Experience of the compounds given in the specification e.g. LRPI-1.1, LRPI-2.1, LRPI-3.1 and LRPI-4.1.

Alternatively, screening or diagnosing a.liver response in a subject, or Alternatively, screening or diagnosing a.liver response in a subject, or monitoring the effect of a drug or therapy administered to a subject, or monitoring the effect of a drug or therapy administered to a subject, or more consecutive nucleotides complementary to a nucleotide sequence encoding an LPRI with RNA obtained from a biological sample from the conject or with cDNA copied from the RNA, where the contacting occurs under conditions that permit hybridisation, if any, between the probe subject or with a previously determined the hybridisation, if any, can the nucleotide sequence, and comparing the hybridisation, if any, between the probe and the nucleotide sequence, with the hybridisation, if any, between the probe cannot be above step, with the hybridisation attented is useful for screening or diagnosing a liver response in a subject, identifying a subject a risk of developing liver response in a subject, identifying a subject a risk of developing liver response in a subject, identifying a subject a risk of developing liver response in a subject, conditioning the effect of therapy administered to a subject having liver response. This is the amino acid sequence of a liver response-associated constructing the effect of therapy administered to a subject having liver response. This is the amino acid sequence of a liver response-associated constructions the construction of more LRPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walchli S, Arigoni F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL70819 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2003; 2003WO-EP050385
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Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial; Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor; phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity; inflammation; multiple sclerosis; angiogenesis-dependent disease; infectious disease; appetite suppressor; congestive heart failure; neurodegenerative disease; ischamia; demyelinating disease; PTPIB; protein tyrosine phosphatase 1B.
                                                                      The present invention relates to phosphopetides that inhibit protein tyrosine phosphose are useful as a medicament or for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity, inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g. solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used diseases, ischaeming congestive heart failure, meurodegenerative diseases, ischaemic events of the brain or demyelinating diseases. The present sequence is one such phosphopetide from protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to phosphopeptides that inhibit protein tyrosine phosphatase. The phosphopeptides are useful as a medicament or for manufacturing a medicament for the treatment and/or prevention of cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity, inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New phosphopeptides that inhibit protein tyrosine phosphatases, useful for manufacturing a medicament for preventing or treating e.g. cancer, diabetes, obesity, inflammation, multiple sclerosis or infectious
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                                                                                                                                                                                                                                                                                                                                     Score 30; DB 8; Length 15;
Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                   Example 1; SEQ ID NO 17; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL70905 standard; peptide; 15 AA.
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTP1B phosphopeptide #19.
                                                                                                                                                                                                                                                                                                                                                      Local Similarity 71.4
                                                                                                                                                                                                                                                             phosphatase 1B (PTP1B)
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YNAYQVD 12
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us-09-831-253f-4.rag

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solid cancer or metastatic cancer) or infectious disease (i.e. leishmaniasis), or as a suppressor of appetite. These may also be used for preventing or treating congestive heart failure, neurodegenerative diseases, ischaemic events of the brain or demyelinating diseases. The present sequence is one such phosphopeptide from protein tyrosine phosphatase 1B (PTP1B).
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Sequence 15 AA;

0; Gaps Query Match

40.0%; Score 30; DB 8; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels

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4 YSAFQVD 10 |:|:||| 9 YNAYQVD 15

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Search completed: November 14, 2004, 12:02:09 Job time: 46.4043 secs

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US-09-842-776A-30 US-110-211-462-91 US-110-084-813-974 US-110-084-813-975 US-10-09-80-148-2839 US-10-094-813-1029 US-10-084-813-1029 US-10-084-813-1022 US-10-084-813-1022 US-10-084-813-1024 US-10-084-813-1024 US-10-1084-813-781 US-10-084-813-781 US-10-084-813-782 US-10-084-813-782 US-10-084-813-783 US-10-084-813-783 US-10-084-813-784 US-10-084-813-784 US-10-084-813-784 US-10-084-813-784 US-10-084-813-785 US-10-084-813-784 US-10-084-813-785 US-10-084-813-785 US-10-084-813-785 US-10-084-813-785 US-10-084-813-785 US-10-084-813-788 US-10-084-813-788

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APPLICANT: Kiyosue, Tomohiro
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Yadegari, Ramin
APPLICANT: Harada, John
APPLICANT: Gloldberg, Robert B.
TITLE OF INVENTION: Pruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
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COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
) OPERATING SYSTEM: PC-DOS/MS-DOS
) CURRENT APPLICATION DATP:
; CURRENT APPLICATION DATP:
; APPLICATION NUMBER: US/09/071,838

TIING DATE: 01-MAY-1998

TILING DATE: 01-MAY-1998
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 173, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-071-838-173
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Sequence 173, App
Sequence 173, App
Sequence 125, App
Sequence 312, App
Sequence 201443,
Sequence 685, App
Sequence 622, App
Sequence 711, Ap
Sequence 711, Ap
Sequence 25, Appl
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Sequence 3991, Ap
                                                                                                              November 14, 2004, 12:03:21; Search time 35.4255 Seconds (without alignments) 149.815 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-10-213-512-173

1 US-10-230-880-125

1 US-10-286-394-335

5 US-10-48-599-201443

6 US-10-481-180-692

6 US-10-481-180-692

4 US-10-166-698-7411

6 US-10-167-538-25

4 US-10-167-538-25

US-09-880-748-3097

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                                                                                                                                                                                                                                                                                                                  1568699 segs, 353819137 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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US-10-285-394-332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fischer, Robert L.
APPLICANT: Chad, Nir
APPLICANT: Chad, Nir
APPLICANT: Kyoue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
FILE REFERENCE: 0213070-086110US
CURRENT APPLICATION NUMBER: US/10/213,512
CURRENT FILING DATE: 2002-08-06
                                                                                                                                                                                                                                                                                          Gaps
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Publication No. US20030190705A1

GENERAL INFORMATION:
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: MSQUEAK, LUIS A.
TITLE OP INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71758/58066
CURRENT APPLICATION NUMBER: US/10/230, 880
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: 09/990,586
RRIOR APPLICATION NUMBER: 60/343,306
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Pred. No. 16;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                       Query Match 48.0%; Score 36; DB 9; Length 17; Best Local Similarity 46.7%; Pred. No. 16; Matches 7; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/177,206
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: US/09/071,838
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-213-512-173
; Sequence 173, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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Best Local Similarity 46.7
Matches 7; Conservative
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                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-173
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Sequence 201443, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
APPLICANT: C
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Fublication No. US20030228883A1

GENERAL INFORMATION:

APPLICANT: AMACHER, DAVID E.

APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI

APPLICANT: HOUT, GORDON DUANE

APPLICANT: STIGER, THOMAS R.

TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE

FILE REFERENCE: POA-003.01

CURRENT FALING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/335,964

PRIOR APPLICATION NUMBER: 60/335,964

PRIOR APPLICATION NUMBER: 60/335,964

SOFTWARE: PATENTION OF 2.11

SOFTWARE: PATENTIN OF 2.12

SOFTWARE: PATENTIN OF 2.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32;
Pred. No.
PRIOR FILING DATE: 2001-10-29
PRIOR PELLING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.1
LEGOGID NO 125
LEGNGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.3%;
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Best Local Similarity 42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNPYSAFQVDIIVD 14
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                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-230-880-125
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ORGANISM: Glycine max
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Matches 5; Conserv
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US-10-424-599-201443
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2 NP--YSAFQVDII 12
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FGCFKIDIWV 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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US-10-106-698-7411
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APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: HUMAN SERVICES
APPLICANT: Valenzuela, Jesus G.
APPLICANT: Valenzuela, Jesus G.
APPLICANT: Rahawi, Shaden
APPLICANT: Rahawi, Shaden
APPLICANT: Rahawi, Shaden
APPLICANT: Ribeiro, Jose M. C.
TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
TITLE OF INVENTION: UNMBER: US/10/481,180
CURRENT APPLICATION NUMBER: US 60/299,391
PRIOR APPLICATION NUMBER: US 60/299,391
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 884
SSEQ ID NOS: 884
SSEQ ID NO 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 692, Application US/10481180
Sequence 692, Application US/10481180
Fublication No. US20040171821A1
GENERAL INPORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: HUMAN SERVICES
APPLICANT: Valencuela Jusus G.
APPLICANT: Valencuela Jusus G.
APPLICANT: Rahawi, Shaden
APPLICANT: Rahawi, Shaden
APPLICANT: Rahawi, Shaden
APPLICANT: Ribairo, Jose M. C.
ITILE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
TITLE OF INVENTION: OF SELECTING AND USES THEREOF
FILE REFERENCE: 4239-67347
CURRENT APPLICATION NUMBER: US/10/481,180
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                                                                Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                              4; Indels
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_23928C.1.pep
US-10-424-599-201443
                                                                Score 31; DB 15;
Pred. No. 1.5e+02;
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Pred. No. 2.1e+02;
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                                                                                                              5; Mismatches
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                                                                                                                                                                                                                                                                                                                  Sequence 685, Application US/10481180
Publication No. US20040171821A1
GENERAL INFORMATION:
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Best Local Similarity 46.2%;
                                                                41.3%;
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                                             3 PYSAFQVDIIVDI 15
                                                                                                                                                                                        2 PYATFPMTILISE 14
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GENERAL INFORMATION 105/10106698

Publication No. US20030109690A1

Publication No. US20030109690A1

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid

TITLE OF INVENTION WINBER: US/10/106,698

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: PT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR PILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PatentIN Ver. 3.0

SEQ ID NO 7411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-7411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence, NOTE OTHER INFORMATION: Synthetic Construct
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Pred. No. 2.6e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 30; DB 16; Length 19; 46.2%; Pred. No. 2.2e+02; tive 2; Mismatches 3; Indels
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,391
PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 884
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 692
LENGTH: 19
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; Publication No. US20040171821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 40.0%;
Matches 4; Conservative
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Sequence 43921, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 38.7%; Score 29; DB 14; Length 20; Best Local Similarity 62.5%; Pred. No. 3.6e+02; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: No. US20030113749A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO. 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 69/632,366
PRIOR APPLICATION NUMBER: US 69/632,366
PRIOR PLILING DATE: 2000-09-03
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-130
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
                                                             INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PYSAFQVD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 PHSVFNVD 20
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US-09-864-761-43921
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Jessen, Tlum H.
Xu, Charatig Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
                                                   APPLICANT: SIZER, JOSE M. C.
TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
TITLE OF INVENTION: OF SELECTING AND USES THEREOF
FILE REFERENCE: 4239-67347
CURRENT APPLICATION NUMBER: US/10/481,180
CURRENT PELING DATE: 2003-12-17
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,391
PRIOR APPLICATION NUMBER: US 60/299,391
PRIOR APPLICATION NUMBER: US 60/299,391
NUMBER OF SEQ ID NOS: 884
SOFTWARE: FREEED for Windows Version 4.0
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CUNDIVIKI: U.28A4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,538
FILING DATE: 04-Jun-2002
CLASSIFICATION NUMBER: US/08/630,052
FILING DATE: CURNOWN>
APPLICATION NUMBER: US/08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/504,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence; NOTE OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%; Score 30; DB 16; Length 23;
46.2%; Pred. No. 2.7e+02;
tive 2; Mismatches 3; Indels
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REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/10162536
Publication No. US20030113749A1
GENERAL INFORMATION:
APPLICANT: Brent, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Karen F. Lech
Kamhawi, Shaden
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Best Local Similarity 46.2
Matches 6; Conservative
                              Sacks, David
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US-10-162-538-25
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LENGTH: 23
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 100.4
....neg 5; Conservative
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Best Local Similarity 50.0
Best Local 4; Conservative
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CRGANISM: Homo sapiens
US-10-293-418-3097
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PP523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/31,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
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                                                                                                                                               OTHER INFORMATION: MAP TO ACO06227.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
                                                                                                                                                                                                                                                                                                                                               38.7%; Score 29; DB 9; Length 22; 54.5%; Pred. No. 4e+02; tive 1; Mismatches 4; Indels
          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Publication No. US20030223996A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3097
LENGTH: 10
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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US-09-880-748-3097
                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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                           SEQ ID NO 43921
LENGTH: 22
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WS-09-842-776A-30

WS-09-842-776
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OTHER INFORMATION: Complementarity determining region (CDR3) of an
OTHER INFORMATION: antibody heavy chain directed to a beta-urease
OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-30
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37.3%; Score 28; DB 14; Length 10; 50.0%; Pred. No. 2.5e+02; ive 2; Mismatches 2; Indels
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## APPLICANT: Bob Biotechnology, Inc.
### TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
### TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
### TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
### CINCARENT FILING DATE: 1003-02-13
### PRIOR FILING DATE: 2001-02-14
### PRIOR FILING DATE: 2001-02-24
### PRIOR FILING DATE: 2001-02-25
### PRIOR FILING DATE: 2001-03-25
### PRIOR FILING DATE: 2001-03-25
### PRIOR FILING DATE: 2001-11-29
### PRIOR PRIOR DATE: 2001-11-29
### PRIOR PRIOR DATE: 2001-21-462-91
### PRIOR PRIOR DATE: 2001-21-462-91
### PRIOR PRIOR DATE: 2001-314,244
### PRIOR FILING DATE: 2001-11-29
### PRIOR PRIOR DATE: 2001-314,244
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Search completed: November 14, 2004, 12:26:59 Job time : 35.4255 sec8

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Rattus sp.
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NON TER
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Matches
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Q7RA82
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O9qvi0 rattus sp.
O9qvi0 rattus sp.
O76mm5 leuryphary
O76mm54 bacillus th
O7xb05 zea mays (m
O7xb05 zea mays (m
O7x761 zea mays (m
O7x761 zea mays (m
O7x761 zea mays (m
O7x761 zea mays (m
O7x806 zea mays (m
O7xb06 zea mays (m
O7xb07 zea mays (m
O7xb07 zea mays (m
O7xb07 zea mays (m
O7xb01 zea mays (m
O9140 zea mays (m
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                                                                           November 14, 2004, 11:57:26; Search time 40.0532 Seconds (without alignments) 215.479 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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09qvb2
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07r1b6
09qv59
5.1.6
Compugen Ltd.
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version :
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Maximum Match 100%
Listing first 45 summaries
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07RA82
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P81801
Q7XB06
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Q68988
Q8R1Q1
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091U21
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Q33429
Q9UC43
Q9R5G0
Q7RKF7
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Gapop 10.0 , Gapext 0.5
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GenCore (c) 1993
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2: uniprot_trembl:*
                                                       using
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Match Length DB
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length: 23
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Perfect score:
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Maximum DB E
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      32
      23.5
      31.3
      19
      2
      Q8SEPP
      Q88kW8
      Genista tyr

      34
      23.5
      31.3
      19
      2
      Q8SKX1
      Q88kX1
      Genista gas

      35
      23.5
      31.3
      19
      2
      Q8SKX5
      Q88kX3
      Genista gas

      36
      23.5
      31.3
      19
      2
      Q8SKX5
      Genista don

      37
      23.5
      31.3
      19
      2
      Q8SKX5
      Genista don

      38
      23.5
      31.3
      19
      2
      Q8SKX5
      Genista don

      40
      23
      30.7
      10
      2
      Q76MX9
      Q78hb6
      Gnista don

      41
      23
      30.7
      10
      2
      Q76MX9
      Q76mX9
      Gnista don

      42
      23
      30.7
      10
      2
      BAB97148
      Bab87148
      Bab87149
      Bab87156
      Bab87156
      Butyphary

      44
      23
      30.7
      10
      2
      BAB87156
      Bab87156
      Butyphary

      45
      23
      30.7
      14
      2
      Q98582
      Q98582
      Q97518
      V97518
      V97518
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## ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=92031479; PubMed=1931964;
Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
Structural and functional correlates of sucrase-alpha-dextrinase in intact brush border membranes.";
Biochemistry 30:10399-10408(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=17XNL;
STRAIN=17XNL;
PubMed=12368865;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29; DB 2; Length 18; Pred. No. 5.1e+02; 3; Mismatches 3; Indels
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 21, Last annotation update)
Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
                                                                                                                                                                                                                                                                                                                                                                                                                        68FF1ABA87B24E49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
  18
                                                                                                                                                                                                                                                                                                                                                                                                                           2122 MW;
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ilarity 45.5%;
Conservative
PRELIMINARY;
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SNPISELRVEV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
Les 5; Conserv
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"The type 2 capsule locus of Streptococcus pneumoniae.";
J. Bacteriol. 181:2652-2654 (1999).
                                                                                      STRAIN=D39;
Pearce B.J., Iannelli F., Pozzi G.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026471; AAD10169.1; -.
                                                                                                                                                                                                                                                                                   Conservative
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                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PY00315;
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SEQUENCE
                                                                                                                                                                                                                                           Query Match
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090VI0;
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Q7RSP0;
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                                                                                                      "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:122-519(2002).

-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Damjanov A., Damjanov I.;
Isolation of serine protease from granulated metrial gland cells
"Isolation of serine protease from polichos biflorus.";
J. Reprod. Fertil. 95:679-684 (1992).
SEQUENCE 20 AA; 2290 MW; 0A304F61A22C500D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
Wararyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10095;
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Pred. No. 1.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                           37.3%; Score 28; DB 2; Length 9; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indels
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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                                                                                   9 AA; 1001 MW; 4687A5AB476455B7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Last annotation update)
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STRAIN=D39;
MEDLINE=99214122; Pubmed=10198036;
Iannelli F., Pearce B.J., Pozzi G.;
                                                                                                                                                                                                              preliminary data.
EMBL; AABL01002263; EAA18865.1; -.
Hypothetical protein.
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MEDLINE=93020730; Pubmed=1404084;
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5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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les 5; Conserv
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Best Local Similarity
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NCBI_TaxID=1313;
                                                                                      Carucci D.J.;
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Q98550;
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Matches
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Matches
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Q9QVB2
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Sucrase-alpha-dextrinase subunit alpha, S-D subunit alpha
                                                 Length 12;
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                                            Score 26; DB 2; Length 12;
Pred. No. 1.2e+03;
4; Mismatches 2; Indels
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SEQUENCE 16 AA; 1979 MW; A87BC2C996760379 CRC64;
90A979D2B2B9CDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
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Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                            16 AA
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                                              34.7%;
12 AA; 1405 MW;
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33.3%;
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10 AA; 1261 MW;
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Similarity 62.5%;
5; Conservative
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                                                                                                                                                                            Local Similarity 62.9
                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                              Mitochondrion.
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Q7M154;
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          Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                          Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.; "Structural and functional correlates of sucrase-alpha-dextrinase in intact brush border membranes."; Biochemistry 30:10399-10408(1991).
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                                                                                                                                                                              Gaps
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Excenzyme (Fragment).
Clostridium botulinum.
Bacteria, Firmicutes; Clostridia, Clostridiales; Clostridiaceae,
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                                                                                                                                                        Score 26; DB 2; Length 19;
Pred. No. 1.9e+03;
4; Mismatches 2; Indels
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NON TER 19 19
SEQUENCE 19 AA; 2119 MW; C84537919B7149D1 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                     22 AA.
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Mitochondrion.
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                                                          SEQUENCE.
MEDLINE=92031479; PubMed=1931964;
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                                                                                                                                                         34.7%;
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                                                                                                                                                                              4; Conservative
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nes 5; Conservative
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5 FSALEISLIV 14
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Best Local Similarity
                                   NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1491;
                                                                                                                                                                                                                                                                                                                                                                                                                         exoenzyme C3.";
                                                                                                                                                                                                                                                                                                                                                    Clostridium.
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Q76MM5
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[1] SEQUENCE FROM N.A.
MEDILINE=22967687; PubMed=12949142;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
"Evolution of the deep-sea gulper eel mitochondrial genomes: largescale gene rearrangements originated within the eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
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"Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";
Mol. Biol. Evol. 20:1917-1924(2003).
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Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Eurypharyngidae; Eurypharynx.
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Pred. No. 1.5e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
GO: GO:0005739; C:mitochondrion; IEA.
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10 AA; 1261 MW; 357BFE29C682DB47 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
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Last sequence update)
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Pred. No. 1.5e+03;
0; Mismatches 3;
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Palaisa K.A., Morgante M., Williams M., Rafalski A.;
"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1795-1806(2003).
EMBL; AX300592; AAPS5331.1; -.
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 4, Last annotation update)
Puromycin-hydrolyzi\ng enzyme (EC 3.-.-.) (Fragment).
                                                                                                                                                                                                                                                                                                                                                           9B1E0AA05615C325 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Pred. No. 2e+03;
2; Mismatches
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Pred. No. 2e+03;
1; Mismatches
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STRAIN-W-17, and W-50;
MEDLINE=22779048; PubMed=12897253;
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54.5%;
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STRAIN=JCM4673 / KCC S-0673;
PubMed=9538199;
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Q79A22;
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"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Cell 15:1795-1806 (2003).
EMBL, AY300568; AAP55307.1; -.
                                                                                                                                                                                                        "Bacillus thuringiensis sep. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.";

FEBS Lett. 232:249-251(1988).

PIR; S00616; S00616.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                           Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,
Stepanov V.M.;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Parasporal crystal protein, wax moth-specific (Fragment).
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 2; Length 11;
Pred. No. 1.7e+03;
1; Mismatches 0; Indels
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
05-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
Name-psy2;
2ea mays (Maize).
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80.0%;
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Similarity 54.5%;
6; Conservative
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5 NNPYS 9
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Q7X761
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Nishimura M., Mateuo H.; Sudiyama M.;

"Blasticidin S-producing Streptomyces morookaensis possesses an enzyme activity with hydrolyzes puromycin.";

"Elasticidin S-producing Streptomyces morookaensis possesses an enzyme activity with hydrolyzes puromycin.";

"EMMS Microbiol. Lett. 132:95-1001(1995).

"THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL.

"TEMPERATURE IS 45 DEGREES CELSIUS.

"I ENZYME REGULATION: GAINOPEPTIDASE ACTIVITY.

"I-ENZYME REGULATION: STIMULAFIED BY DIT. STRONGLY INHIBITED BY ZINC.

ION, FERROUS ION, CUPRIC ION, MERCHY ION, N-BROWOSUCCINIMIDE AND N-ETHYLMALEIMIDE. PARTIALLY INHIBITED BY COBALT ION.

"I MISCELLANEOUS HAS AN ISOBLECTRIC POINT OF 6.4.

GO; GO:0016787; F-hydrolase activity; IEA.

"Minopeptidase; Hydrolase.
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Nishimura M., Matsuo H., Nakamura A., Sugiyama M.; "Purification and characterization of a puromycin-hydrolyzing enzyme from blasticidin S-producing Streptomyces morookaensis."; "J. Biochem. 123:47-252 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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MEDLINE=22779048; PubMed=12897253;
Palaisa K.A., Morgante M., Williams M., Rafalski A.;
"Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";
Plant Call 15:1795-1806 (2003).
EMBL; AY300558; AAP55297.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Virizio; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 2.1e+03;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           NON TER 14 14 SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 AA; 1869 MW; BEB5FAA056459674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene synthase 2 (Fragment).
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                                                                                         AND FUNCTION
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 54.5
Matches 6, Conservative
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                                                                                       CHARACTERIZATION,
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Zea mays (Maize)
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NON TER
SEQUENCE
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Search completed: November 14, 2004, 12:07:31 Job time: 42.0532 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds (without alignments) 155.938 Million cell updates/sec Run on:

US-09-831-253F-4 75 1 SNPYSAFQVDIIVDI 15 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

4495 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79: \* 1: pir1: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	calcium-activated	potassium channel	L-serine dehydrata	duodenase - bovine	exoenzyme C3 - Clo	parasporal crystal	formylmethanofuran	exo-poly-alpha-gal	arsenite oxidase I	glandular kallikre	L-2,4-diaminobutyr	vespakinin M - hor	27K protein A 3.4/	allatostatin - tob	interphotoreceptor	glutamate-1-semial	trypsin (EC 3.4.21	DNA topoisomerase	brain-associated s	interphotoreceptor	hypothetical prote	interphotoreceptor		osomal pro	unidentified 85K p	protein QF200039 -	D-galactose-bindin	G leader pep	Ig heavy chain DJ
SOMMENDS	ID	C39800	PS0446	S16376	869371	805236	800616	A58946	A48968	A45138	A54326	B44854	A61360	PS0185	A61612	G24417	A48301	A61334	S43834	A61392	D24417	A85659	C24417	PT0229	836899	PC2369	PA0061	S29174	B26930	PH1313
	ength DB	!					11 2					14 2						17 2										15 2		19 2
ф	Query Match Length	41.3	41.3	36.0	36.0	34.7	33.3	33.3	33.3	32.0	30.7	30.7	29.3	29.3	29.3	9	29.3	29.3	29.3	29.3	29.3	29.3	29.3	28.0		28.0	Θ.	28.0	æ,	28.0
	Score	31	31	27	27	26	25	25	25	24	23	23	22	22	22	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21
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interphotoreceptor	lysophospholipase	mast cell proteina	probable transcrip	Ig heavy chain DJ	Ig heavy chain V r	enamelin i - bovin	MUC1 enhancer bind	hypothetical prote	NADH2 dehydrogenas	methane monooxygen	MHC class II histo	pregnancy-specific	ribosomal protein	glycoprotein H-a -	tubulin alpha-chai
F24417	S27351	A35646	B90996	PH1361	PH1729	S10784	A59018	808209	PQ0778	A48179	179432	A44524	836898	A40795	865612
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28.0	28.0	28.0	28.0	28.0	28.0	26.7	26.7	26.7	26.7	26.7	26.7	26.7	25.3	25.3	25.3
21	21	21	21	21	21	20	20	20	20	20	70	20	19	19	13
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1 C39800 calcium-activated potassium channel, alternate exon B - fruit fly (Drosophila melanogas Calcium-activated potassium channel, alternate exon B - fruit fly (Drosophila melanogas C; Species: Drosophila melanogaster C; Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004 C; Accession: C39800 R; Atkinson, N. S.; Robertson, G.A.; Ganetzky, B. Science 253, 551-55, 1991 A; Title: A component of calcium-activated potassium channels encoded by the Drosophila A; Reference number: A39800; WUID:91313401; PMID:1857984 A; Reference number: A39800; WUID:91313401; PMID:1857984 A; Retension: C39800 A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr A; Molecule type: mRNA A; Residues: 1-22 cATKs A; Cross-references: UNIPROT:Q03720 C; Genetics: A; Gene: Flysase:slo A; Cross-references: Flysase:FBgn0003429
	Query Match Best Local Similarity 44.4%; Pred. No. 46; Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
	Qy 1 SNPYSAFQV 9         : :   :   Db 6 ANPYAGYQL 14
	RESULT 2 potassium channel protein Slo II - fruit fly (Drosophila melanogaster) (fragment) c;Species: Drosophila melanogaster c;Species: Drosophila melanogaster c;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004 c;Accession: PS0446 R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bon Neuron 9, 209-216, 1992 A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs A;Reference number: JH0697; MUID:92360298; PMID:1497890 A;Accession: PS0446 A;Accession: PS0440 A;Accession: PS0446 A;Accession
_	es 4; Conservative 4; Mismat

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parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria:
                                                                                                                                                                                                                                                                                                                                                               R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M. FBBS Lett. 232, 249-251, 1988
A;Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotox
A;Reference number: S00615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Cross-references: UNIPROT: 07M154
C, Comment: This toxin is effective against the larvae of Galleria melonella (greater wax C, Superfamily: parasporal crystal protein
C, Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium t
NAILernate names: formylmethanofuran dehydrogenase (molybdenum) chain B (misidentificat
C;Species: Methanobacterium thermoautotrophicum
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A58946
R;Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
Birchemer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
Bur. J. Biochem. 234, 910-920, 1995
A;Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoautof A;Reference number: S63519; MUID:96163477; PMID:8575452
A;Accession: A58946
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Appl. Environ. Microbiol. 59, 828-836, 1993
A;Title: Isolation and characterization of an extracellular glycosylated protein comple:
A;Reference number: A48968; MUID:93243739; PMID:8481009
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                                                                                                                                                                                                                                                                 N,Alternate names: delta-endotoxin; parasporal crystal protein positive chain
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A;Residues: 1-17 <HOC>
A;Note: the authors identify this peptide as the amino terminus of chain B,
C;Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exo-poly-alpha-galacturonosidase (EC 3.2.1.82) - Clostridium thermosaccharol N;Alternate names: exo-poly-alpha-galacturonate hydrolase (C)Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum (C)Date: 21-Jan.1994 #sequence_revision 18-Nov-1994 #text_change 06-Dec-1996 C;Accession: A48968
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Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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Pred. No. 4e+02;
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Indels
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Pred. No. 2.5e+02;
Mismatches
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A, Molecule type: protein
A, Residues: 1-11 < CHE>
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                                                                                                                                                                                                                             C;Species: Peptostreptococcus asaccharolyticus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S16376
R;Grabowski, R.; Buckel, W.
Eur. J. Biochem. 199, 89-94, 1991
A;Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat A;Reference number: S16224; MUID:91293139; PMID:2065681
A;Accession: S16376
A;Status: preliminary
A;Accession: Lype: protein
A;Redeule type: protein
A;Residues: 1-16 < EUR.>
A;Cross-references: UNIPROT:P33074
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C;Daces 24-Uul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004.
C;Dacession: S69371
R;Zamolodchikova, T.S.; Vorotyntseva, T.I.; Antonov, V.K.
Eur. J. Biochem. 227, 866-872, 1995
A;Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal A;Reference number: S69371; MUID:95172075; PMID:7867648
A;Rocession: S69371
A;Rocientle type: protein
A;Residues: 1-21 < ZAM>
A;Cross-references: UNIPROT:Q9GLN2
C;Superfamily: trypsin; trypsin homology
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C,Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C,Accession: S05236
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                                                                                                                                                                                                            - Peptostreptococcus asaccharolyticus
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A;Title: Immuno-crossreactivity between botulinum neurotoxin type Cl A;Reference number: S05236; MUID:89338716; PMID:2474453
A;Reference trype: Protein
A;Reference trype: Totalinum neurotoxin type Cl A;Reference number: S05236
A;Reference number: G708-A;Residues: 1-22 - TORA-A;Residues: 1-22 - TORA-A;Residues: 1-22 - TORA-A;Residues: UNIPROT:Q7M0L1
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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45.5%;
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Similarity 83.3%;
5; Conservative
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7 ANPYAGYQL 15
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                        SNPYSAFOV
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Best Local Similarity
Matches 5; Conserv
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1 YSAFEV 6
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C;Species: Vespa mandarinia
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A61360
R;Kishimura, H; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2886-2897, 1976
A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ve
A;Reference number: A61360; MUID:77114342; PMID:1017116
RiYamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.
J. Gen. Microbiol. 138, 1461-1465, 1992
A.Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from A; Reference number: A44854; MUID:92381494; PMID:1512577
A; Accession: B44884
A; Molecule type: protein
A; Residues: 1-14 <YAM>A; Residues: 1-14 <YAM>A; Residues: 1-14 <YAM>A; Residues: 1-12 <YAMA>A; 
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C;Species: Oryza sativa (rice)
C;Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995
C;Accession: PS0185
R;Kamo, M.; Tsugita, A.
Bubmitted to JIPID, June 1991
A;Reference number: PS0184
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C;Superfamily: unassigned animal peptides
C;Keywords: hydroxyproline; venom
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental
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66.7%; Pred. No. 7.4e+02;
iive 2; Mismatches 0;
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42.9%; Pred. No. 9.4e+02;
iive 3; Mismatches 1;
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A61612
allatostatin - tobacco hornworm
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Best Local Similarity 50.0%
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Matches 4; Conservative
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Matches 3; Conservative
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-12 <KIS>
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TAFEVD 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arsenite oxidase II - Alcaligenes faecalis (fragment)
C;Species: Alcaligenes faecalis
C;Species: Alcaligenes faecalis
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45138
R;Anderson, G.L.; Williams, J.; Hille, R.
J. Biol. Chem. 267, 23674-23682, 1992
A;Title: The purification and characterization of arsenite oxidase from Alcaligenes faec
A;Reference number: A45138; WUID:93054722; PMID:1331097
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R; Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.
R; Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.
A; Title: Identification and androgen-regulated expression of two major human glandular A; Reference number: A54326; MUID:92324494; PMID:1726490
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C;Species: Homo sapiens (man)
C;Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                Gaps
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                                    A;Molecule type: protein
A;Residues: 1-23 <VAN.
A;Note: sequence extracted from NCBI backbone (NCBIP:130462)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                                                                                                                                                              33.3%; Score 25; DB 2; Length 23; 57.1%; Pred. No. 5.7e+02; ative 2; Mismatches 1; Indels
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A;Molecule type: protein
A;Residues: 1-18 AMD>
A;Cross-references: UNIPROT:09R5G0
A;Note: sequence extracted from NCBI backbone (NCBIP:118544)
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3 YAAFEYD 9
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SHPYS 6
   A;Status: preliminary
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RiFong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B. FEBS Lett. 205, 309-312, 1986
A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10 A;Reference number: A91365; MUID:86301171; PMID:3743780
                                                                C;Accession: A61612
R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. U.S.A. 88, 9452, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 9452, 1991
A;Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta. A;Reference number: A61612, MUID:92052112; PMID:1946359
A;Accession: A61612
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <KRA>
A;Cross-references: UNIPROT:P42559
C;Keywords: neuropeptide; pyroglutamic acid
C;Keywords: neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C;Species: Manduca sexta (tobacco hornworm)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
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N/Alternate names: interstitial retinol-binding protein
C/Species: Cricetinae gen. sp. (hamster)
C/Bate: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C/Accession: G24417
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29.3%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels
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29.3%; Score 22; DB 2; Length 15; Best Local Similarity 33.3%; Pred. No. 1.2e+03; Matches 3; Conservative 4; Mismatches 2; Indels
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Molecule type: protein
A,Residues: 1-15 <PON
A,Cross-references: UNIPROT:P12665
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Search completed: November 14, 2004, 12:03:11 Job time : 10.2553 secs

| | :::|: 7 FQPSLVLDM 15 HIV pepti Human pap Human pap

Adk08459 Adk08095

Abg34100 Abg34094 Aaw13936

Abp14228 | Abp19690 | Adl17639 |

Antigenic Charligenic CDR-3 and Mark Mode BRIN B62 BERIN PDE HIV Depti HIV Depti HIV A02 BHIV A01 BHIV A01 BHIV A01 BHIV A01 BHIV A02 BBHIV A02

Aam22772 Aam22747 Abp16598 Abp14239

HIV HIV HIV HIV

Abp18424 Abp22273 1 Abp11937 1

Abp19680 B Abp19688 B Abp14253 B

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of simulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
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Borras Cuesta F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor inhibitory peptide #3
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             AAM22800
ADK08459
ADK08459
ABG34100
ABG34100
ABG34094
ABG34100
ABG34100
ABF1659
AAM22772
AAM22772
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY92947 standard; peptide; 12
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WO200031135-A1
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                                                                                                        November 14, 2004, 12:37:20 ; Search time 155 Seconds (without alignments) 27.773 Million cell updates/sec
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Copyright (c) 1993 - 2004
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
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Maximum DB seq length: 12
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Post-processing:

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Human 161

Human Human Human

ADE66432 ADE67609 ADE70007 ADE67387

AAW63878 ADE67540

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Result

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AAY93008

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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY22945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
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Borras Cuesta P;
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Pred. No. 0.00091;
0; Mismatches 0; Indels
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                        AAY93009 standard; peptide; 12 AA.
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AAY93094
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100.0%; Score 63; DB 3; Lo
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0;
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Borras Cuesta F;
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Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides ANY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                       Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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    Borras Cuesta F;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                       Borras Cuesta F;
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                             Hepatotropic, antagonist; transforming growth factor betal; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Pred. No. 1.7e+06;
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Pred. No.
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                                                                                       disease, specifically cirrhosis
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100.0%;
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Cuesta F;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Pred. No. 1.7e+06;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, specifically cirrhosis
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75.0%;
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Conservative
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                                                                                                    1 TSL---MIWIMM
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Best Local Similarity
Matches 9; Conserv
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                                                                                              Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                  Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
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                                                                                    Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor, liver, extracellular matrix degradation inhibitor, mimetope, cirrhosis.
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                                          Transforming growth factor inhibitory peptide P141.
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
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Best Local Similarity
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Borras Cuesta F;
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1 DATMIW
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                                                                                                                                                                              Homo sapiens
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Gaps

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Indels

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Prieto Valtuena J;

Rattus sp

AAY93010;

RESULT 10 AAY93010

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Matches

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95WO-US006315.
                         46.0%;
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                                                    6; Conservative
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Ruhland-Fritsch B;
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Best Local Similarity
Matches 4; Conserv
                                                                            1 TSLDATM 7
                                     Best Local Similarity
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                                                                                              TSLDATV
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Sequence 7 AA;
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                                                                                                                                                                                                                    21-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                           23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lower alkyl
                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                            AAR86068;
                          Query Match
                                                                                                                                       RESULT 13
AAR86068
                                                  Matches
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                                                          The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial animo acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAV2945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides AAW45983-W456025 are based on portions of somatostatin, somatostatin receptors (SSTR) and insulin-like growth factor binding proteins (IGFBP). They are capable of increasing weight gain, birth weight, growth rates, milk production, levels of circulating insulin, IGF-I and IGF-III, fibre production and muscle weight. They may be used to modulate carbohydrate metabolism and in treatment of diabetes. The oil carrier may be used for delivery of the peptides
useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New non-naturally occurring peptide(s) - which are based on portions of somatostatin, somatostatin receptors and insulin-like growth factor binding protein.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone, receptor, antibody, vaccine, immunogen, somatostatin, IGF, insulin-like growth factor binding protein, ILGFBP, SSTR, diabetes, somatostatin receptor, insulin-like growth factor.
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                                                                                                                                                                                                                                           Score 31.5; DB 3; Length 9; Pred. No. 1.7e+06; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #41 based on human SSTR 4 (residues 282-290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingston DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 9; 136pp; English.
                                    Disclosure; Page 31; 86pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NORT-) NORTHSTAR BIOLOGICALS PTY
                                                                                                                                                                                                                                                                                                                                                                                      AAW46010 standard; peptide; 7 AA.
                                                                                                                                                                             expression systems) encoding the disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-AU000312
                                                                                                                                                                                                                                            h 50.0%;
Similarity 75.0%;
9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Peptides AAR86024-R86236 are examples of peptides and their mimetics that bind to endothelial leukocyte adhesion molecule (ELAM)-1. This molecule is a member of the selectin family of receptors and is involved in binding of leukocytes to the vascular endothelial wall prior to carravasation of the leukocyte, e.g. to a site of inflammation. The peptides bind pref. to E-selectin but may also bind i. or P-selectin, and can be used to treat conditions mediated by E-selectin, e.g. inflammatory conditions. The peptides have strong affinity for the selectin receptors and inhibit the binding of the sialyl Lewis (Sin-x) part of cell surface glycoproteins to E-selectin. The peptide are small, generally less than 2 kb, have an ICSO of up to 100 micromole against binding of HL60 cells to ELAM-1) have one or more peptide linkages replaced by CH2OC(O)NR, phosphonate, CH2SOZNR, CH2NR, CON(R6), or NHCONH linkages where R = H or substituted N- and C-termini e.g. succinimido, N-benzyloxycarbonyl or N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin; receptor; leukocyte; vascular wall; endothelium; extravasation; inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide (s) that bind to endothelial leukocyte adhesion molecule 1 -useful for treating inflammation and other B-selectin mediated diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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80.0%; Pred. No. 2.38+02;
ive 1; Mismatches 0; Indels
                                                                                    0; Indels
Score 29; DB 2; Length 7; Pred. No. 1.7e+06;
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                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR86068 standard; peptide; 12 AA.
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Peptide(s) that bind to ELAM-1 - for research or therapeutic use.
                                     endothelial leukocyte adhesion molecule 1; ELAM-1; HL60 cells;
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 8; 39pp; English.
                                                                                                                                                                                                                                    (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                                                                                                                                                                                                Dower WJ, Martens CL,
           ELAM-1 binding peptide.
                                                                                                                                                                                                                                                                                            WPI; 1997-372109/34.
                                                     selectin receptor
                                                                                                                                                                 16-FEB-1995;
                                                                                                                                                                                             06-MAY-1992;
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                                                                                                                                      15-JUL-1997.
                                                                                                           US5648458-A.
                                                                                Synthetic.
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peptides AAR86024-R86236 are examples of peptides and their mimetics that bind to endothelial leukocyte adhesion molecule (ELAM)-1. This molecule to a member of the selectin family of receptors and is involved in binding of leukocytes to the vascular endothelial wall prior to extravasation of the leukocyte, e.g. to a site of inflammation. The peptides bind pref. to B-selectin but may also bind L- or P-selectin, and can be used to treat conditions mediated by E-selectin, e.g. inflammatory conditions. The peptides have strong affanity for the selectin receptors and inhibit the binding of the sialyl Lewis (SLe-x) part of cell surface glycoproteins to B-selectin. The peptide are small, generallyl less than 2 kD, have an IC50 of up to 100 micromole against binding of H40 cells to ELAM-1, have one or more peptide linkages replaced by CH2OC(0)NR, phosphonate, CH2SC2NR, CA2NR, CON(R6), or NHCONH linkages where R = H or substituted N- and C-termini e.g. succinimido, N-benzyloxycarbonyl or N-CNA lower alkyl cpds
                                                                                                                                                           Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin; receptor; leukocyte; vascular wall; endothelium; extravasation; inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide (s) that bind to endothelial leukocyte adhesion molecule 1 -useful for treating inflammation and other E-selectin mediated diseases.
                                                                                                                                                                                                                                                                                                                                                                                          Dower WJ, Koller KJ, Lee J, Martens CL;
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66.7%; Pred. No. 2.3e+02;
tive 1; Mismatches 1;
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                                                  AAR86065 standard; peptide; 12 AA
                                                                                                                                      Anti-ELAM-1 binding peptide #42.
                                                                                                                                                                                                                                                                                                                                                                (AFFY-) AFFYMAX TECHNOLOGIES NV
                                                                                                                                                                                                                                                                                                         95WO-US006315.
                                                                                                                                                                                                                                                                                                                                    94US-00241054.
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-010687/01.
                                                                                                                                                                                                                                                                                                                                                                                          Barrett RW, Cwirla
Ruhland-Fritsch B;
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                                                                                                                                                                                                                      Synthetic.
                                                                              AAR86065;
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                                       AAR8606
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Barrett RW;

Cwirla SE,

92US-00881395. 93US-00057295. 95US-00390156

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                                 adhesion molecule-1 (ELAM-1). The compounds include a lead peptide HITWOLLWAWAY ("AFFY 4"; AAW2655) discovered using random peptide diversity generating systems (e.g. "peptides on plasmids" or "peptides on phage" systems) and peptides ecreened from a library designed to produce peptides which differ from the lead peptides on plasmids" or "peptides on peptides which block the binding of HiGO cells to ELAM-1 are the preferred compounds of the invention. These peptides generally contain the core sequence WXXLWXXM or WXXLWXX-NIE, where X is any amino acid. The peptides are used as research tools for studying the biological role of ELAM-1 and other selectin receptors; to evaluate factors that may influence or be influenced by cell adhesion; in the development of other compounds that bind to ELAM-1; and for blocking adhesion of leukocytes to cells expressing ELAM-1; and for blocking adhesion of leukocytes to overproduction of Cytokines. The present sequence represents an example
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The invention provides compounds that bind to endothelial leukocyte
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Job time : 157 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a peptide of the invention
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LWTMM 11
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Gaps

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Matches

7 MIWTWM 12

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6 MLWNWM 11

Local Similarity

AAW26904 standard; peptide; 12 AA.

AAW26904

27-NOV-1997 (first entry)

AAW26904;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 33624;
BDDLINE=BDLINE=BST1824
Spratt D.A. Greenman J., Schaffer A.G.;
"Capnocytophaga gingivalis aminopeptidase: a potential virulence
                                                                                                                                                                                                Aas87902 }
Aas87903 }
Aas87904 }
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-!- COFACTOR: Requires magnesium or calcium.
Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;
 26rac5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capnocytophaga gingivalis.
Bacteria, Bacteroidetes, Flavobacteria, Flavobacteriales,
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Pred. No. 1.2e+03;
1; Mismatches 2; Indels
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10 Aa; 1306 MW; 00COA6DB43772694 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Aminopeptidase (EC 3.4.11.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                   10 AA
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QGRACS
QGRACS
QGRAD3
QGRAD3
QGRAB2
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QT7899
QT7891
QT7891
AAS87900
AAS87903
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NCBI_TaxID=1017;
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Similarity 50.0%;
3; Conservative
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01-MAY_2000 (TrEMBLrel. 13,
05-JUL_2004 (TrEMBLrel. 27,
Fas antigen (CD95 antigen) (
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P80474;
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Q9UELO;
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Jatropha multifida (Physic nut).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Malpighiales, Euphorbiaceae, Crotonoideae, Jatropheae,
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01-07N-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Arch. Biochem. Biophys. 316:572-584(1995)
PIR; S69159; S69159.
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SEQÜENCE 10 AA; 873 MW; D88458DDDDAB;
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Ravanel S., Droux M. Doure P
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                                                                                                                                            "Transcription Stimulaton of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection."; J. Biol. Chem. 270:18007-18012(1995).
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                                                                                                                                                                                                                                                                      Muschen M., Re D., Brauninger A., Wolf J., Hansmann M.L., Diehl V., Kuppers R., Rajewsky K.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Unidentified 5.7/35k protein (Fragment)
Oryza sativa (Rice)
Bukaryoza, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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K MEDLINE=22404279; PubMed=12516573;
Kurth J., Perniok A., Schmitz R., Iking-Konert C., Chiorazzi N.,
Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
T plasmablaste from systemic mutations in the CD95 gene of
T plasmablaste from systemic lupus erythematosus patients and
autoantibody-producing cell lines.";
Eur. J. Immunol. 32:3785-3792(2002).
R EMBL, 913968; BAA20850.1;
R EMBL, AJZ79011; CAC35539.1;
R EMBL, AJZ79012; CAC35540.1;
R EMBL, AJZ79012; CAC35541.1;
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                                            TIŠSUE-Blood;
MEDLINE-95355401; PubWed-7543095;
Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
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"A rice protein library; a data-file of
two-dimensional electrophoresis.";
Theor. Appl. Genet. 86:935-942(1993).
PIR; PQ0731; PQ0731.
NON TER 1 1 11
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophylales; Amaranthaceae; Spinacia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ravanel S., Droux M., Douce R., Methionine biosynthesis in higher plants. I. Purification and characterization of cystathionine gamma-synthase from spinach
Score 20; DB 1; Length 10; Pred. No. 6.7e+03; Mismatches 0; Indels
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RESULT 6

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Eukaryotâ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=98008057; PubMed=9581555;
HOSPITAL A., Joule C., Cherif D., Day R., Cohen P.;
HOSPITAL V., Prat A., Joulle C., Cherif D., Day R., Cohen P.;
HOMEN and rat testis express two mRNA species encoding varients of NRD convertase, a metalloendopeptidase of the insulinase family.";
Biochem. J. 327:773-779(1997).
EMBL; X93208; CAA63695.1; -.
SEQUENCE 8 AA; 886 MW; EA7EAIBIADC5A5B6 CRC64;
                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L., Geysen J.J.G.H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ488208; CAD32561.1; -.
NON TER 8
SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                           8 AA.
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Name=ORF1;
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Q9H3Y3
ID Q9H3Y3
AC Q9H3Y3;
DT 01-MAR-2
DT 01-MAR-2
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01-NOV-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
02-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
02-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
04-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
05-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
06-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
07-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
07-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
07-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
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MEDLINE=98115113; PubMed=9649539;

MEDLINE=98115113; PubMed=9649539;

Figuacoa F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

Figuacoa F., Sultmann H., Klein J.,

"Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.",

"Linkage relationships and haplotype polymorphism among cichlid MHC
Genetics 149:1527-1537(1998).

EMBL; AF050006; AAC41345.1; -.

NON_TER 1 1

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SEQÜENCE 11 AA, 1399 MW; 3F47DB7A772685A3 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=92129337; PubMed=1733949; Stracke M.L., Krutzsch H.C., Unsworth B.J., Arestad A., Cioce V., Stracke M.L., Krutzsch H.C., Unsworth B.J., Arestad A., Cioce V., Schiffmann B., Liotta L.A.; "Identification, purification, and partial sequence analysis of autotaxin, a novel motility-stimulating protein."; J. Biol. Chem. 267:2524-2529(1992).
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Pred. No. 1.1e+04;
2; Mismatches 0; Indels
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30.2%; Score 19; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels
    2; Indels
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NON TER 12 12
SEQÜENCE 12 AA; 1493 MW; 433482B3F335A1A7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
AUTOTAXIN (Fragment)
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NCBI_TaxID=8128;
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Name-beta fibrinogen;
Antilophia galeata (Helmeted manakin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Antilophia.
NCBI_TaxID=208054;
Chiroxiphia caudata.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Passeriformes, Pipridae, Chiroxiphia.
NCBI_TaxID=196027;
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Marini M.A., Hackett S.J.,
"A Multifaceted Approach to the Characterization of an Intergeneric
"A Multifaceted Approach from Brazil.";
Auk 119:1114-1120(2002).
BMBL; AX136616; AAN1693.1; -.
NON TER 9 9
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta fibrinogen (Fragment).
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66.7%;
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Best Local Similarity 66.77,
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Name=beta fibrinogen;
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Q801K1;
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Q801K1
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AC 0801K
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OC Archo
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  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ33931.1. (Novel protein with a Kunitz/Bovine pancreatic trypsin inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide core' domains) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
80ta fibrinogen (Fragment).
Name-beta fibrinogen;
11icura militaris (pin-tailed manakin).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Ilicura.
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MEDLINE=88118956; PubMed=2963134;
Buckley K.J., Hayashi M.;
Buckley K.J., Hayashi M.;
"Role of premeture translational termination in the regulation of expression of the phi X174 lysis gene.";
"Mol. Biol. 198:599-607(1987).
EMBL; X07089; GAA30668.1; -.
NON TER
                                                                                  Name-dJ461P17.1;
Homo sapiens (Hunan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                      Lloyd D.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121778; CAB76844.1; -.
NON TER 9 9
SEQÜENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             038366;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E gene product (Fragment).
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Viruses; ssDNA viruses; Microviridae; Microvirus.
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Marini M.A., Hackett S.J.;
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1 MWTV 4
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WADLINE-93151962; PubMed-8427629;
A Stratilova E., Markovic O., Skrovinova D., Rexova-Benkova L.,
Jornvall H.;
Thectinase Aspergillus sp. polygalacturonase: multiplicity,
Thivergence, and structural patterns linking fungal, bacterial, and
The plant polygalacturonases ";
The divergence, and structural patterns linking fungal, bacterial, and
The plant polygalacturonases ";
The divergence, and structural patterns linking fungal, bacterial, and
The plant polygalacturonases activity; IEA.

The plant polygalacturonase activity; IEA.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amortation update)
Polygalacturonase (EC 3.2.1.15) IV (Fragment).
Appergillus sp.
Ekpergillus sp.
Eurotiales Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales, Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Query Match 28.6%; Score 18; DB 2; Length 9; Best Local Similarity 66.7%; Pred. No. 1.8e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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7 WTL 9
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Search completed: November 14, 2004, 12:54:38 Job time : 188 secs

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Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-758-128-44
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Sequence 44, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 44, Appl
Sequence 642, Appl
Sequence 662, Appl
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31.219 Million cell updates/sec
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                                                                                                                                                          November 14, 2004, 12:54:46; Search time 136 Seconds
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1: \cgn2 \( \) \cgn2 \( \) \( \) \( \) \cgn2 \( \) \( \) \cgn2 \( \) \( \) \cgn
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-758-198-44
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US-09-75-198-44
US-09-661-661-44
US-10-062-109A-642
US-10-105-48BA-642
US-10-105-48BA-642
US-10-105-48BA-685
US-10-105-25A-685
US-10-135-25A-685
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Maximum Match 100%
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Match Length DB
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Maximum DB seq length: 12
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Sequence 501, Appli
Sequence 44, Appli
Sequence 69, Appl
Sequence 14, Appl
Sequence 151, App
Sequence 61, App
                    Sequence 79, Appl
Sequence 501, Appl
Sequence 7, Appli
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US-09-755-109-7
                                       US-09-823-829-44
US-09-821-823-44
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US-10-609-217-151
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US-10-61-761-151
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US-10-62-151
US-10-62-151
US-10-182-252A-617
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US-10-182-252A-658
US-10-182-11-551
US-10-005-180A-13
US-10-162-252A-630
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APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: WESTBROOK: Simon L.
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REPERENGE: 0.6786/0214
CURRENT APPLICATION NUMBER: US/09/758,128
CURRENT FILING DATE: 2001-01-12
PRIOR FILING DATE: 1990-02-05
PRIOR FILING DATE: 1990-02-05
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PACENTIN VET. 2.0
SOFTWARE: PACENTIN VET. 2.0
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Pred. No. 1.4e+06;
1; Mismatches 0; Indels
; Sequence 41, Application US/09758128; Patent No. US20020107187A1; GENERAL INFORMATION:
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85.7%;
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ORGANISM: Homo sapiens
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SEQ ID NO 41
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Patent No. US20020169116A1

GENERAL INFORMATION:
APPLICANT: GERRATY, No. US20020169116A1man L.
APPLICANT: MESTERROWE: Simon L.
TITLE OF INVENTION: MODULATION THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: PEPTIDES, ANTHBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214

CURRENT APPLICATION NUMBER: US/09/758,426

CURRENT FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: O9/194,218

PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARR: PATENTIN VER. 2.0

SOFTWARR: PATENTIN VER. 2.0
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                                                                  APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020107187Alman L.
APPLICANT: GERRATY, No. US20020107187Alman L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214
CURRENT APPLICATION NUMBER: US/09/758,128
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-25
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
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Pred. No. 1.4e+06;
1; Mismatches 0; Indels
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Sequence 44, Application US/09758128
Patent No. US20020107187A1
GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
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Matches 6; Conserv
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ORGANISM: Rat
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US-09-758-426-41
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Sequence 44, Application US/09758426
Patent No. US20020169116A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: GERRATY, No. US20020169116A1man L.

US-09-758-426-44

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JAPPLICANT: GERRATY, No. US20020187925Alman L.

APPLICANT: GERRATY, No. US20020187925Alman L.

APPLICANT: GERRATY, No. US20020187925Alman L.

APPLICANT: GERRATY, No. US20020187925Alman L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT PILING DATE: ARALIER FILING DATE: 1999-0-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312

PRIOR APPLICATION NUMBER: EARLIER PLING DATE: 1997-05-25

PRIOR FILING DATE: BARLIER FILING DATE: 1997-05-22

PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATCHTIN VET. 2.0
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APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
FILE REFERENCE: 016786/0214 LOS, 426
CURRENT APPLICATION NUMBER: US/09/758,426
CURRENT FILING DATE: 2001-01-12
PRIOR PLING DATE: 1999-0-05
PRIOR FILING DATE: 1999-0-05
PRIOR FILING DATE: 1999-0-05
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1 Sequence 44, Application US/09758198

2 Sequence 44, Application US/09758198

3 Sequence 44, Application US/0202187925A1

5 PUBLICANT NO. US2020187925A1

5 APPLICANT: GERRATY NO. US2020187925A1man L.

7 APPLICANT: WESTBROOK, Simon L.

7 APPLICANT: WESTBROOK, Simon L.

7 ITILE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

7 ITILE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
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; Sequence 41, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
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US-09-758-426-44
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Gaps

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APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Entitled 16192F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REPERENCE: 51158-20062.01
FILE REPERENCE: 51158-20062.01
FURRENT APPLICATION NUMBER: US/10/062,109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR APPLICATION NUMBER: US 10/005,480
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.00
CURRENT APPLICATION NUMBER: US/10/005,480A
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44.4%; Pred. No. 2.9e+02;
iive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                  Score 29; DB 10; Length 7; Pred. No. 1.4e+06; 1; Mismatches 0; Indels
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; Publication No. US20030191073A1
; GENERAL INFORMATION:
  PRIOR APPLICATION NUMBER: AU PN9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Agensys
APPLICANT: Challita-Bid, Pia M. APPLICANT: Raitano, Arthur B. APPLICANT: Faris, Mary
                      PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.4
Matches 4; Conservative
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US-10-062-109A-642
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TCVESTRIW 9
                                                                                                                                                               ; ORGANISM: Rattus sp. US-09-861-661-44
                                                                                                                                                                                                                                                                                                                                  1 TSLDATM 7
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                                                                                             SEQ ID NO 44
LENGTH: 7
                                                                                                                                            TYPE: PRT
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Fublication No. US20030045676A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, DAVID J.
APPLICANT: WESTBROOK, SIMON L.
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
FLIE REFERENCE: 054270/0135;
CURRENT APPLICATION NUMBER: US/09/861,661
CURRENT PELING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1996-05-25
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR APPLICATION NUMBER: AU PN9990
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PALENT NOS: 59
SOFTWARE: PALENT NOS: 59
SOFTWARE: PALENT NOS: 59
SEQ ID NO 41
         CURRENT APPLICATION NUMBER: US/09/758,198

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218

PRIOR FILING DATE: BARLIER FILING DATE: 1999-02-05

PRIOR FILING DATE: BARLIER FILING DATE: 1997-05-22

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22

PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22

NUMBER: APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22

SEQ ID NOS: 58

SOFTWARE: PALENTIN Ver. 2.0
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Publication No. US20030045676A1
GENERAL INFORMATION:
APPLICANT: KINGSTON, DAVID J.
APPLICANT: GERRATY, NORMAN L.
APPLICANT: WESTBROOK, SIMON L.
TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF FILE REFERENCE: 624270/0135
CURRENT APPLICATION NUMBER: US/09/861,661
CURRENT FILING DATE: 2001-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 9; I
Pred. No. 1.4e+06;
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PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
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Best Local Similarity 85...
Fra 6; Conservative
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Best Local Similarity 85...
Section 6; Conservative
FILE REFERENCE: 016786/0214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41
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| TSLDATV 7
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1 TSLDATV 7
                                                                                                                                                                                                                                                                                                                             ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                     US-09-758-198-44
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Gaps

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TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto CITY: Palo Alto COUNTRY: US
                                                                                                                                                                                                         39.7%; Score 25; DB 14; Length 8; 37.5%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.7%; Score 25; DB 14; Length 9; 80.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/10357935
Publication No. US20030165958A1
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
GOATE, Alison Mary
MULLAN, Michael John
CHARTIER-HARLIN, Marie-Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Liebeschuetz, Joe
REGISTRATION UNDBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-Jun-1995
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
COMPUTER: DEADER
COMPUTER: DEADER
COMPUTER: DEADER
COMPUTER: DEADER
APPLICATION DATA:
APPLICATION NUMBER: US/10/357,935
FILING DATE: 03-Feb-2003
CLASSIFICATION 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

NOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-357-935-20
                                                                       TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 326-;
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS
                                                                                                               FEATURE:
COTHER INFORMATION: Synthetic US-10-190-082-602
                                                                                                                                                                                                                                                         3; Conservative
  NUMBER OF SEQ ID NOS: 683
SEQ ID NO 602
LENGTH: 8
                                                                                                                                                                                                                                                                                                      4 DATMIWIM 11
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Matches 3; Conserva
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DETSVWVL 8
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Best Local Similarity
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US-10-357-935-20
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APPLICANT: BUUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: 2003-04-10
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Publication No. US20030148264A1

GENERAL INFORMATION

APPLICANT: Lawrence A.

APPLICANT: Sidhu, Sachdev S.

APPLICANT: Held, Helke A.

ITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

FILE REFERENCE: P1905R1

CURRENT APPLICATION NUMBER: US/10/190,082

CURRENT FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 60/303,634

PRIOR FILING DATE: 2001-07-06
                                                                                                                                                                                                                                 Pred. No. 2.96
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR PILING DATE: 2001-01-29
PRIOR PLING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR PLING DATE: 2000-01-31
PRIOR PLING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 642
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 685, Application US/10182252A Publication No. US20040072162A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FOMSGAARD, ANDERS
                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3
Matches 3; Conservative
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1 IQAIVVWTV 9
                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapien
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1 TCVESTRIW 9
                                                                                                                                                            US-10-005-480A-642
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Gaps

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TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-657
                                                                                                                                                                       Query Match 39.7%; Score 25; DB 15; Length 9; Best Local Similarity 42.9%; Pred. No. 1.4e+06; Matches 3; Conservative 3; Mismatches 1; Indels
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3 AIVVWTL 9
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APPLICANT: FUNDAMA, SOREN
APPLICANT: GORBET, STAVIER
APPLICANT: GORBET, STAVIER
APPLICANT: GORBET, STAVIER
APPLICANT: GORBET, STAVIER
APPLICANT: LAUGNOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT APPLICATION NUMBER: DCT/DK01/00059
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 657
                                                                                                                                                                                                                                                                                                               APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV DEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: LIVE DEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: COWINCL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR APPLICATION NUMBER: PF 00610017.6
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
NUMBER OF SEQ ID NOS: 1388
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     0; Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-632
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39.7%; Score 25; DB 15; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels
  0; Indels
  1; Mismatches
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                                                                                                                                                                                                                     Application US/10182252A o. US20040072162A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
4; Conservative
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3 AIVVWTL 9
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2 ATVIW 6
                                                5 ATMIW 9
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Sequence 632, Ap
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LENGTH: 9
  Matches
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APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Cwirla, Steven E. APPLICANT: Cwirla, Steven E. APPLICANT: Dower, William J. APPLICANT: Dower, William J. APPLICANT: Bartens, Christine L. APPLICANT: Martens, Christine L. APPLICANT: Martens, Christine L. APPLICANT: Ruland-Fritsch, Beatrice APPLICANT: Ruland-Fritsch, Beatrice TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                              Sequence
Sequence
Sequence
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Sequence
Sequence
Sequence
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Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 06-MAY-1992
ATPARTAN NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATPARTATION NUMBER: 30,113
REFERENCE/CATION NUMBER: 30,113
REFERENCE/CATION NUMBER: 30,113
REFERENCE/CATION NUMBER: 000324-002
TELECOMMUNICATION NOMBER: 000324-002
US-08-439-817-78
US-08-445-508-95
US-08-485-508-95
US-08-485-508-95
US-09-823-823-44
US-09-823-886C-170
US-08-974-685-180
US-08-974-685-180
US-08-974-685-180
US-08-974-685-180
US-08-974-685-180
US-08-974-685-180
US-08-444-818-563
US-09-149-476-551
US-08-444-818-563
US-09-147-95-46
US-09-177-929-24
US-09-620-091-443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Burns, Doane, Swecker & Mathis
699 Prince Street
                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                        Sequence 50, Application US/08241054
Patent No. 5643873
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 69
                                                                                                                                                                                                                                                                                                                                                          US-08-241-054-50
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                               November 14, 2004, 12:46:25 ; Search time 36 Seconds (without alignments) 22:106 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30,
Sequence 33,
Sequence 41,
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Sequence 53,
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Sequence 5
Sequence 5
Sequence 6
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Sequence 5
Sequence 6
Sequence 9
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Sequence 2
Sequence 2
Sequence 2
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Sequence 7
Sequence 5
Sequence 5
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                                                                                                                                                                                                                                                                                                 130155
                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-241-054-50
US-08-241-054-53
US-08-390-156A-22
US-08-390-156A-22
US-08-390-156A-61
US-08-439-817-33
US-08-439-817-33
US-08-495-817-41
US-08-495-508-50
US-08-495-508-50
US-08-465-508-50
US-08-465-508-50
US-08-464-250-20
US-08-464-250-20
US-08-444-2108B-7
US-08-411-054-55
US-08-241-054-55
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-439-817-35
US-08-439-817-75
                                                                                                                                                                                                                                                                 478139 seqs, 66318000 residues
            GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                      sw model
                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                     - protein search, using
                                                                                                                                                                                        1 TSLDATMIWTMM 12
                                                                                                                                                           US-09-831-253F-3
63
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Match Length
                           Copyright
                                                                                                                                                                                                                                                                                                                           | length: 0
| length: 12
                                                                                                                                                                                                                                                                                                                             seq
                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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Maximum DB s
                                                                     OM protein
                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                  Searched:
                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
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GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Coller, Kerry J.
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Solectins Including Endothelium Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTWARE: PatentIN Release #1.0, Version #1.25
SOSTWARE: PatentIN BATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 1.mAY-1994
CLASSIFICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
RPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1993
RPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
APPLICATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
                                                                                                                        Sequence 61, Application US/08241054
Patent No. 5643873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Sw
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 IWTMM 12
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7 LWTMM 11
  LWTMM 11
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                                                                         RESULT 3
US-08-241-054-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Barret, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Cwirla, Steven E. APPLICANT: Cwirla, Steven E. APPLICANT: Cwirla, William J. APPLICANT: Koller, Kerry J. APPLICANT: Lee, Jung APPLICANT: Martens, Christine L. APPLICANT: Ruhland-Fritsch, Beatrice APPLICANT: Selectins Including Endothelium Leukocyte Adhesion TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                   Score 28; DB 1; Length 12;
Pred. No. 1e+02;
                                                                                                                                                     1; Indels
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ZIP: 2213

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 06-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATORNEY AGENT INFORMATION:
NAME: Gerald F. Swies
REGISTRATION NUMBER: 30,113
REFERENCE/POCKET NUMBER: 30,113
REFERENCE/POCKET NUMBER: 30,113
REFERENCE/POCKET NUMBER: 000324-002
TELEPHONE: 415-84-7700
TELEPHONE: 415-84-7700
TELEPHONE: 12-84-8275
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/08241054
Patent No. 5643873
                                                                                                 h 44.4%;
Similarity 66.7%;
4; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-241-054-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-241-054-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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STRANDEDNESS: si
                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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Gaps

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8 IWTMM 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CMITA, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALDEASSE: ALLYMAX IECHIOLOGIES, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: 4011 fornia
CUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: PATENTIN Release #1.0, Version #1.25
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATA: 16-FEB-1996
RILNG DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: SWAISS, GAFTAIR.
NAME: SWAISS, GAFTAIR.
REGISTRATION NUMBER: 30,133
                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING APPLICATION NUMBER: US 08/057,295
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING APPLICATION NUMBER: US 07/881,395
ATTORNEY/AGENT INFORMATION:
NAME: SWISS Gerald F.
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELEFRAX: 415-496-2300
TANDEMENT: OFF 17 NO. 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B: Affymax Technologies, N.V.
4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 61, Application US/08390156A Patent No. 5648458 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-390-156A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-390-156A-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Bower, William J.
APPLICANT: Dower, William J.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
CORRESPONDENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind tartic OF INVENTION: Belam 1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                      WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION NUMBER: US 08/057,295
PRILING DATE: 05-MAY-1993
PRILING DATE: 05-MAY-1993
PRILING DATE: 05-MAY-1993
PRILING DATE: 06-MAY-1993
PRILING DATE: 06-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Swies, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Affymax Technologies, N.V. STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/08390156A Patent No. 5648458 GENERAL INFORMATION: APPLICANT: Cwirla, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 415-424-0832
INPORMATION FOR SEQ 1D NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                       STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 MIWTMM 12
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GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwilar, William J.
APPLICANT: Cwilar, William J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Molecule I (ELAM-1)
CORRESPONDENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSE: Affigmax Technologies, NV
                                                                                                                                                                        Gaps
                                                                                                                                                                        ö
                                                                                                                   Score 28; DB 1; Length 12;
Pred. No. 1e+02;
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                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 06-MAY-1993
FILING DATE: 06-MAY-1992
ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
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AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
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AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
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AMADE: ATTONNEY/AGENT INFORMATION:
AMADE: ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-046/1056.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/08439817 Patent No. 5728802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLY TECHNOL CITY AND AND COLTY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
                                                                                                                      44.48;
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80.0%;
                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
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                                                                      US-08-439-817-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Malland-Pritsch, Beatrice
TITLE OF INVENTION: Selectine Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                           DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                         0; Indels
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ZIP: 94304
ZUNE 94304
ZUNE 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
FILING DATE: 11-MAY-1994
FILING DATE: 05-MAY-1993
FILING DATE: 05-MAY-1993
FILING DATE: 05-MAY-1993
FILING DATE: 06-MAY-1993
FILING DATE: 06-MAY-1993
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 14 ALUER D.
ATTORNEY/AGENT INFORMATION:
NAMME: SEEVEND ALUER D.
TELEPHONE: 415-436-2300
TELEPRAXION NUMBER: 36,691
TELEPHONE: 415-424-0832
INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acida
TYPE: amino acida
                                                                                                                                                                                                                                                                                         Score 28; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/08439817
Patent No. 5728802
TELECOMMUNICATION INFORMATION
               TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Peptid
TITLE OF INVENTION: Select
TITLE OF INVENTION: Molecu
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRRESS:
ADDRESSEE: Affymax Techn
                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                        8 IWTMM 12
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7 LWTMM 11
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APPLICANT: Dower, William J.
APPLICANT: Moler, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1e+02;
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PP: 000324-002/1056
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                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
                                      ; Sequence 50, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-485-508-53
Sequence 53, Application US/08485508
Patent No. 5786322
GENERAL INFORMATION:
                                                                                          Barrett, Ronald W.
Cwirla, Steven E.
Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single

// MOLECULE TYPE: peptide
US-08-485-508-50
                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 MLWNWM 11
                        US-08-485-508-50
                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                         APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dec, William J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Selectins and Compounds That Bind
TITLE OF INVENTION: Molecule I (BLAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1e+02;
1; Mismatches 0; Indels
   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/081,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000324-046/1056.1
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Affymax Technologies, NV STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             Sequence 41, Application US/08439817 Patent No. 5728802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REPERENCE/DOCKET NUMBER: 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.48;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 12 amino acids
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-439-817-41
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Barrett
                                   8 IWTMM 12
                                                                    LWTWM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 IWTMM 12
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                                                                                                                                          US-08-439-817-41
Matches
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APPLICANT: Barrett, Ronald W.

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RESULT 13
US-08-385-9
US-08-385-9
I Sequence 9, Application US/08396385
Fatent No. 601349
GENERAL INFORMATION:
APPLICANT: Schlom, Jeffrey
APPLICANT: Panicall, Dennis
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES
TITLE OF INVENTION: THEREOF
INVERSPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: & CUSHMAN
STREET: 130 WATER STREET

STREET: 130 WATER STREET
Peptides and Compounds That Bind
Selectins Including Endothelial Leukocyte Adhesion
Molecule I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,508

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION: 514

PRIOR APPLICATION STA

PRIOR APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION WHERE: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION WHERE: US 08/057,295

FILING APPLICATION WHERE: US 07/881,395

RICHARD APPLICATION NUMBER: US 07/881,395

RICHARD APPLICATION NUMBER: US 07/881,395

RICHARD APPLICATION NUMBER: OS 07/881,395

ATTORNEY/AGENT INFORMATION:

ANDER OF MANALES OF MAY-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         000324-002/1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                              E: Affymax Technologies, NV 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stevens, Lauren L. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                    TITLE OF INVENTION: Pept
TITLE OF INVENTION: Sele
TITLE OF INVENTION: MOLE
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Tec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-485-508-61
                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LWTMM 11
                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                       Lee, Jung
Martene, Christine L.
Rubland-Fritsch, Beatrice
MENTION: Peptides and Compounds That Bind
VENTION: Selectins Including Endothelial Leukocyte Adhesion
VENTION: Molecule I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/485,508

FILING DATE: 11-MAY-1994

CLASSIFICATION NUMBER: US 08/21,054

FILING DATE: 11-MAY-1994

CLASSIFICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/057,295

FILING DATE: 06-MAY-1993

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000324-002/1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrett, Ronald W.
Cwirla, Steven E.
Dower, William J.
Koller, Kerry J.
Lee, Jung
Martens, Christine L.
Ruhland-Fritsch, Beatrice
                                                                                                                                                                                                                                                                   3: Affymax Technologies, NV
4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 61, Application US/08485508
Patent No. 5786322
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFRENCE/DOCKET NUMBER: 00033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                    Cwirla, Steven E. Dower, William J. Koller, Kerry J.
                                                                                  APPLICANT: Lee, Jung
APPLICANT: Martens, Christ:
APPLICANT: Ruhland-Fritsch,
TITLE OF INVENTION: Peptid
TITLE OF INVENTION: Molecul
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESSE
ADDRESSEE: Affymax Techno
STREET: 4001 Miranda Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 IWTMM 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LWTMM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-485-508-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-485-508-61
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HARDY, John Anthony
APPLICANT: HARDY
APPLICANT: GOATE, Alison Mary
APPLICANT: GUARTHANDAN
APPLICANT: CHARTIER-HARDIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 2; Length 9;
Pred. No. 3.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                     Score 27; DB 3; I
Pred. No. 1.3e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,165
FILING DATE: 21-JAN-1992
CLASSIFICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATPONEY/AGENT INFORMATION:
NAME: Liebeschuetz, Jos
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 16163-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-104-165-20
; Sequence 20, Application US/08104165
; Bettent No. 5877015
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
  ; INFORMATION FOR SEQ ID NO: 9; SEQUENCE CHARACTERISTICS: ; LENGTH: 10 amino acids ; STRANDEDNESS: unknown ; TOPOLICY: unknown ; TOPOLICY: unknown ; US-09-287-221-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.7
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-104-165-20
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         4 DATMIW
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APPLICANT: Schlom, Jeffrey
APPLICANT: Schlom, Jeffrey
APPLICANT: Panicali, Dennis
APPLICANT: Panicali, Dennis
APPLICANT: Panicali, Dennis
APPLICANT: Panicali, Dennis
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ECUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10;
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COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,385
FLING DATE:
FLING DATE:
CLASSIFICATION:
NAME: Resinick, David S.
REGISTRATION NUMBER: 44933
TELEPRATION NUMBER: 44933
TELEPRATION NUMBER: 44933
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TELENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/287,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 3; 1
Pred. No. 1.3e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/396,385
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09287221
Patent No. 6319496
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORING DATE:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFRENCE/DOCKET NUMBER: 4493:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 DATMIW 9
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Search completed: November 14, 2004, 12:55:03 Job time : 37 sece

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 14, 2004, 11:57:25; Search time 7.40425 Seconds (without alignments) 155.938 Million cell updates/sec Run on:

US-09-831-253F-3 63 1 TSLDATMIWTMM 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

4495 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ig H chain V-D-d r Ig H chain V-D-d r	H chain	Ig H chain V-D-J r	Ig H chain V-D-J r	ğ	Ig H chain V-D-J r	killer toxin - yea	rRNA endonuclease	O)	Ig H chain V-D-J r		Ig H chain V-D-J r	hydroxypyruvate re	ATF-43 protein - h	glutamate-ammonia	Ig heavy chain DJ	Ig H chain V-D-J r		Ig heavy chain DJ		RNA-polymerase-ass	alpha-amylase (EC	Ig heavy chain DJ		Ig heavy chain DJ	cystathionine gamm	Ig H chain V-D-J r	T-cell receptor de
ID	PH1612 PH1625	PH1627	PH1613	PH1637	PH1331	PH1630	PQ0007	PC4030	PQ0731	PH1636	PH1594	PH1638	A44921	S40638	T03261	PH1315	PH1620	A35105	PH1358	PH1602	A44139	PH1380	PH1327	PL0192	PH1326	869159	PH1626	A32220
DB	0.0	N	~	N	~	~	0	~	~	7	~	~	~	~	~	~	~	7	~	7	~	~	~	~	~	7	~	~
% Query Match Length	15	14	15	16	17		22	23	11	13		16				19	13	14	20	7	21	20	14	20	20	10	14	18
% Query Match	47.6	44.4	44.4	44.4	41.3	39.7	39.7	39.7	38.1	38.1	38.1	38.1	38.1	38.1	38.1	37.3	٠	36.5	36.5	34.9	34.9	34.1	33.3	. 33,3	33,3	31.7	31.7	31.7
Score	30	28	28	28	26	25	25	25	24	24	24	24	24	24	24	23.5		23				21.5			21	20		20
Result No.	7 7	Э	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

cytochrome P450-C- L-lactate dehydrog probable trp opero	thrABC leader pept T-cell receptor be Ig heavy chain DJ	T cell receptor al Ig heavy chain DJ self-incompatibili	major outer membra Ig heavy chain V r Ig heavy chain CDR	polygalacturonase proton-translocati collecting duct wa	aeg-46.5 protein -
A28702 149422 AC0269	A47057 PT0586 PH1356	PH1769 PH1352 PQ0751	A44927 PH1731 PT0303	D61440 S69123 I51905	154984
000	000	0 0 0	0 0 0	0 0 0	7
19	22 7 14	14 19	20 21 22	10 13	13
31.7	30.2	30.2	30.2	. 28.6 28.6 28.6	28.6
7000	20 13	0 0 0	139	18 18	18
30 32 32	33 4 33 1	36 37 38	39 41 41	4 4 4 5 6 4	45

# ALIGNMENTS

PHIG12

1 G Hohain V-D-J region (wild-type clone 344) - mouse (fragment)

1 G Hohain V-D-J region (wild-type clone 344) - mouse (fragment)

2 Species: Mus musculus (house mouse)

2 Species: Mus musculus (house mouse)

C Species: Musculus (house mouse)

C Species: Musculus (house mouse)

3. Exp. Med. 178, 317-329, 1993

A; Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic.

A; Reference number: PH1580; MUID:93301609; PMID:8315387

A; Molecule type: DNA

A; Mesiducular source: bone marrow pre-B lymphocyte

C; Keywords: immunoglobulin

Gaps ;; 0 Query Match
47.6%; Score 30; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 4; Conservative 2; Mismatches 1; Indels

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4 DATMIWT 10 : ||:|| 9 EVTMLWT 15 g

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RESULT 2
PH1625

Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999
Exp. Med. 178, 317-329, 1993
J. Exp. Med. 178, 317-329, 1993
J. Farberence number: PH1580; MUID:93301609; PMID:8315387
A;McSecasion: PH1625
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-14 < LEVA;Respinental source: bone marrow pre-B lymphocyte.
C;Keywords: immunoglobulin

ö Query Match 44.4%; Score 28; DB 2; Length 14; Best Local Similarity 80.0%; Pred. No. 29; Matches 4; Conservative 1; Mismatches 0; Indels

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Gaps

6 TMIMT 10 ||:|| 10 TMLWT 14 ò g

RESULT 3 PH1627

```
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH1331
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
T;Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1331
A;Molecule type: DNA
A;Residues: 1-17 <WAS>
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig H chain V-D-J region (clone B-less 156) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1630
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less micc. A;Reference number: PH1580; MUID:93301609; PMID:8315387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Killer toxin - yeast (Pichia farinosa) (fragment)

Killer toxin - yeast (Pichia farinosa) (fragment)

CiSpecies: Pichia farinosa

CiSpecies: Pichia farinosa

CiSpecies: Pichia farinosa

CiSpecies: Or-Jun-1990 #text_change 09-Jul-2004

CiAccession: Pg0007

Risuzuki, C.; Nikkuni, S.

Risuzuki, C.; Nikkuni, S.

Risuzuki, C.; Nikkuni, S.

Airitle: Purification and properties of the killer toxin produced by a halotolerant year

Airitle: Purification and properties of the killer toxin produced by a halotolerant year

Airitle: Purification and properties of the killer toxin produced by a halotolerant year

Airitle: Purification and properties of the killer toxin produced by a halotolerant year

Airitle: Purification and properties of the killer toxin produced by a halotolerant year

Airitle: Purification and properties of the killer toxin depends on NaCl or KCl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                  PH1331
Ig heavy chain DJ region (clone C148-106) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 2; ]
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: bone marrow pre-B lymphocyte C, Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                             DB ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                         41.38;
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Best Local Similarity 44.4
Matches 4; Conservative
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Best Local Similarity
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Matches 4; Conser
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A; Residues: 1-17 < LEV>
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Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0.2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1627
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Molecula type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-14 <LEV
A;Residues: 1-14 <LEV
A;Residues: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig H Chain V-D-J region (clone B-less 17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0.2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Molecula type: DNA
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Residues: 1-15 <LEV>
A;Residues: 1-15 <LEV>
A;Reywords: immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Unn-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1637
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PH1637
A;Molecular type: DNA
A;Residues: DNA
A;Residues: 1-16 <LEV>A;Residues: 1-16 <LEV>A;Residues: 1-16 <LEV>A;Residues: immunoglobulin
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Pred. No. 29;
1; Mismatches 0; Indels
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44.4%; Score 28; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     44.4%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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EATTIW 7

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C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999 C;Accession: PH1594 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999 C;Accession: PH1594 #sequence_revision 02-Jun-1994 #text_changes Torres, J.; Leder, P. B. Exp. Mad. 178, 317-329, 1993 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic A;Reference number: PH1580; MUID:93301609; PMID:8315387 A;Accession: PH1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RiLevinson, D.A.; Campos-Torres, J.; Leder, P.
LEXP. Med. 178, 317-329, 1933
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A;Reference number: PH1580; MUID:93301609; PMID:8315387
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R;Chistosardova, L.V.; Lidetrom, M.E.
B;Chistosardova, L.V.; Lidetrom, M.E.
A;Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase
A;Reference number: A44921; MUID:92104992; PMID:1729225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1638
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C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
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A;Residues: 1-20 CCHI>
A;Cross-trences: GB:M81443; NID:g150010; PIDN:AAA25378.1; PID:g150011
A;Note: sequence extracted from NCBI backbone (NCBIN:75202, NCBIP:75203)
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-14 cLEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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Pred. No. 2e+02;
2; Mismatches
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                                                                                                                                                                                                                                        Ig H chain V-D-J region (wild-type clone 149)
C;Species: Mus musculus (house mouse)
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60.0%;
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Best Local Similarity 60.vv,
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Best Local Similarity 66.7
Matches 4; Conservative
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9 ATGLWT 14
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A; Residues: 1-16 < LEV>
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A; Status: preliminary
                                                                   10 MVWT 13
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                                                                                     FRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)

NyAlternate names: nuclease Le3

NyAlternate names: nuclease Le3

Syspecies Lentinula edodes (shiitake mushroom)

C;Species: Lentinula edodes (shiitake mushroom)

C;Date: 21-3u1-1995 #sequence_revision 03-Aug-1995 #text_change 09-Ju1-2004

C;Accession: PC4030 #sequence_revision 03-Aug-1995 #text_change 09-Ju1-2004

C;Accession: PC4030 #sequence_revision 03-Aug-1995 #text_change 09-Ju1-2004

B;Robayashi, H; Inokudhi, N.; Koyama, T.; Tomita, M.; Irie, M.

B;Rosabi, H; Inokudhi, N.; Koyama, T.; Tomita, M.; Irie, M.

B;Rosabi, H; Inokudhi, N.; Koyama, T.; Tomita, M.; Irie, M.

B;Rosabi, H; Inokudi, N.; Koyama, T.; Tomita, M.; Irie, M.

A;Reference number: PC4030; MUD:95337563; PMID:7613009

A;Rosabi PC4030

A;Rosabi P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified 5.7/35K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: p00731
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension A;Reference number: PQ0696
A;Accession: PQ0731
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R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice A;Reference number: PHI580; MUID:93301609; PMID:8315387
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Ig H chain V-D-J region (clone B-less 224) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
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Pred. No. 1.3e+02;
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Pred. No. 1.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.7%; Score 25; DB 2; Length 23; 37.5%; Pred. No. 1.9e+02; Live 3; Mismatches 2; Indels
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A,Residues: 1-13 <LEV>
A,Experimental source: bone marrow pre-B lymphocyte
C,Keywords: immunoglobulin
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A;Molecule type: protein
A;Residues: 1-11 cKOM>
A;Residues: 1-50
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Best Local Similarity 75.0%;
Matches 3; Conservative
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Matches 3; Conservative
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1 ATVVW 5
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RESULT 15
840638
847E-43 protein - human (fragmente)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Toty, No. 1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C.Accesion: $40638
C.Accesion: $40638
A.Title: Identification and functional characterisation of the cellular activating trans
A.Title: Identification and functional characterisation of the cellular activating trans
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38.1%; Score 24; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                   Query Match
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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12 TSLPQTVVMT 21
C; Keywords: oxidoreductase
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Search completed: November 14, 2004, 12:03:10 Job time : 9.40425 secs

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Q92Y81 amitus sp.
Q98817 oryza sativ
Q98818 oryza sativ
Q94W97 leishmania
Q9ur71 lentinula e
P80474 capnocytoph
Q9uel homo sapien
Q7mlu2 oryza sativ
Q51871 azospirillu
Q51871 azospirillu
Q61419 rattus nory
Q61638 xenopus lae
Aa44680 rattus nor
Q92yws jarta phoro
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Q8x128 scaevola pr
Q49132 methylobact
Q0739 nicoctiana t
Q8hum1 uncultured
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Q95n72 equus cabal
Q4861 oryza sativ
Q8ciq0 rattus norv
Q8ha22 bacteriopha
Q9r570 nitrosomona
                                                                                                   November 14, 2004, 11:57:26; Search time 32.0426 Seconds (without alignments) 215.479 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9UELO
Q9UELO
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LIPW AZOBR
Q6LIDL9
Q6LIDL9
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Q8HUM0
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB seq length: 23
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Q9r5e8 bacillus sp Q9twc0 acanthamoeb Q9prf0 oryzias lat Q9zyc bethylidae Q6wa89 myxine glut Q865g9 aotus azara Aq63924 myxine gl Q93r63 yersinia pe P1370 jatropha mu Q7mlj3 spinacia ol Q6vfms photobacter Aar04051 photobacter Aar04054 photobact Aar04054 photobacter	nnce update) ation update) ation update)  cial rearrangement 'hot spot' in  cial rearrangement 'hot spot' in  1.4e+03; ches 3; Indels 0; Gaps 0;  nnce update) ation update) istidine rich protein s; Embryophyta; Tracheophyta; ida; Poales; Poaceae; atagu M., Van der Straeten D.;
Q9RSEB Q9TWC0 Q9TWC0 Q9PRF0 Q9ZYV6 Q6865G9 AAQ63924 Q93R63 LABA_VATWU Q7M1\overline{\text{J}}3 AAR04051 AAR04054 AAS16489 AAS16489	
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factor.",
Microbiology 141:3087-3093(1995).
Microbiology 141:3087-3093(1995).
-!- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N
-!- FUNCTION: Aminopeptidase but not N-terminal blocked ones.
Cerminal amino acid residues but not N-terminal blocked ones.
Optimum activity is measured at pH 7.5. May be important in the nutrition and pathogenesis of the organism in the human oral
                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
5'-mucleotide-forming nuclease (Fragment).
Lentinula edodes (Shitake mushroom) (Lentinus edodes).
Bukaryota; Fungi, Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Lentinula.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95337563; PubMed=7613009;
Kobayashi H., Inokuchi N., Koyama T., Tomita M., Irie M.;
"Purification and characterization of the 2nd 5'-nucleotide-forming
nuclease from Lentinus eddodes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 13624;
MEDILINE=96118234; PubMed=8574402;
Spratt D.A., Greenman J., Schaffer A.G.;
"Capnocytophaga gingivalis aminopeptidase: a potential virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Requires magnesium or calcium.
Aminopeptidase, Calcium, Direct protein sequencing, Hydrolase,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biosci. Biotechnol. Biochem. 59:1169-1171(1995).
PIK, PC4030; PC4030.
InterPro: IPR008947; PLC Nuclease.
SEQUENCE. 23 AA; 2535 \( \text{WW} \); 978082B3B161FCC6 CRC64;
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(Rel. 44, Last annotation update)
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01-0CT-1996 (Rel. 34, Last seq
05-JUL-2004 (Rel. 44, Last ann
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Local Similarity 37.5%;
les 3; Conservative
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10 AA; 1306 MW;
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Matches 3; Conservative
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P80474;
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"Molecular and physiological responses to abscisic acid and salts in roots of salt-sensitive and salt-tolerant Indica rice varieties."; Plant Physiol. 107:177-186(1995). Gramene; 095817; -. SEQUENCE 18 AA; 2094 MW; 0CD245DB237E7520 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.; "Molecular and physiological responses to abscisic acid and salts in rootes of salt-sensitive and salt-tolerant Indica rice varieties."; Plant Physiol. 107:177-186(1995).
Gramene; Q95818; --
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Cathepsin B-like cysteine protease (Fragment).
Leishmania mexicana.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5665;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
40 Kba Pl 815 ABSCISSIC acid-induced protein (Fragment).
60 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.
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MEDLINE=94187801; PubMed=8139620;
MEDLINE=9400. Coombs G.H.;
"Cathepsin B-like cysteine proteases of Leishmania mexicana.";
Mol. Biochem. Parasitol. 62:271-279(1993).
SEQUENCE 20 AA; 2203 MW; FELA260FALDBE41F CRC64;
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MEDLINE-95175599; PubMed=7870812;
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DESVLWT 16
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Length 23; Indels

Score 25; DB 2; I Pred. No. 1.8e+03;

3; Mismatches

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Score 24; DB 1; Length 10; Pred. No. 1.2e+03; 1; Mismatches 2; Indels

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00C0A6DB43772694 CRC64;

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LPW_AZOBR
P50871;
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                                                                                                                                                                                                                                           "Transcription Stimulaton of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection."; J. Biol. Chem. 270:18007-18012(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Muschen M., Re D., Brauninger A., Wolf J., Hansmann M.L., Diehl V.,
Kuppers R., Rajewsky K.;
Kuppers R., Rajewsky K.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified 6.7/35K protein (Fragment).
Oryza sativa (Rice).
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=22404279; PubMed=12516573;

Kurth J., Perniok A., Schmitz R., Iking-Konert C., Chiorazzi N.,

Kurth J., Perniok S., Schmitz R., Iking-Konert C., Chiorazzi N.,

Thompson K.M., Winkler T., Rajewsky K., Kueppers R.,

"Lack of deleterious somatic mutations in the CD95 gene of
plasmablaste from systemic lupus erythematosus patients and
autoantibody-producing cell lines.";

Eur. J. Immunol. 32:3785-3792(2002).
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                                                                                                                                                                                               TISSUB-Blood;
MEDLINE-95355401; PubMed=7543095;
WAGNINS-95355401; Obba Y., Kobayashi N., Takizawa T.,
Nakanishi Y.;
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Pred. No. 1.3e+03;
Or Indels
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01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                               Last sequence update)
Last annotation update)
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                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequer
05-UUL-2004 (TrEMBLrel. 27, Last annote
Fas antigen (CD95 antigen) (Fragment).
                                             PRT;
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EMBL, AJ279011; CAC35539.1; -.
EMBL, AJ279012; CAC35540.1; -.
EMBL, AJ279013; CAC35541.1; -.
EMBL, AJ509179; CAD48920.1; -.
EMBL, AJ509180; CAD48930.1; -.
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60.0%;
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                                             PRELIMINARY;
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                                                                                                                            Homo sapiens (Human)
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3; Conserv
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4 IWTLL 8
                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                 Name=CD95
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SEQUENCE
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Best Local
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Q7M1U2;
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                     RESULT 7
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Comateu S., Kajiwara H., Hirano H.;
"A rice protein library; a data-file of rice proteins separated by two-dimensional electrophoreals.";
Theor. Appl. Genet. 86:935-942(1993).
PIR; PQ0731; PQ0731.
NON_TER 1 1 1
SEQÜENCE 11 AA; 1319 MW; CBE97F0E53277362 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
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                                                                                                                                                                                                                                                 Length 11;
                                                                                                                                                                                                                                            Score 24; DB 2; Length 11;
Pred. No. 1.3e+03;
2; Mismatches 0; Indels
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SEQUENCE 17 AA; 2114 MW; CD42DDEC3724BC8A CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Neural cell adhesion molecule (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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MEDLINE=97094331; PubMed=8939798;
                                                                                                                                                                                                                                            38.1%;
60.0%;
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Trp operon leader peptide.
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Best Local Similarity 60.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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1 ATVVW 5
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=99152621; PubMed=10028295;
Dowton M., Austin A.D.;
Dowton M., Austin A.D.;
TEVOLUTionary dynamics of a mitochondrial rearrangement 'hot spot'
the hymenoptera '';
Mol. Biol. Evol. 16:298-309(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen A., Reyes A., Akeson R.A.;
"Transcription initiation sites and structural organization of the extreme S. region of the rat neural cell adhesion molecule gene.";
MOI. Cell. Biol. 10:3314-3324 (1990).
EMBL; M32612; AA41680.1; -.
Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.,
"The Xenopus NCAM promoter: Appropriate expression in response to
neural inducing signals and identification of a conserved sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
Braconidae; Alysiinae; Aspilota.
NCBI_TaxID=61200;
                                                                                                                                                                           Score 24; DB 2; Length 17;
Pred. No. 2e+03;
2; Mismatches 0; Indels
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                                                            element.";
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L26396; AAA49911.1; -.
NON TER 17 17 ...
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                                                                                                                                           SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-WAR-2004 (TrEMBLrel. 27, Last sequence update) 02-WAR-2004 (TrEMBLrel. 27, Last annotation update) Neural cell adhesion molecule (Fragment).
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome oxidase II (Fragment).
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Pred. No. 2e+03;
2; Mismatches
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STRAIN=Sprague-Dawley;
MEDLINE=90287121; PubMed=1694009;
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Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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7 LIWTL 11
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7 LIWIL 11
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE-90287121; PubMed-1694009;
Chen A., Reyes A., Akeson R.A.;
"Transcription initiation sites and structural organization of the extreme 5' region of the rat neural cell adhesion molecule gene.";
Mol. Cell. Biol. 10:3314-3324 (1990).
EMBL; M32612; AAA41680.1; -.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Johnson A.D., Oveenek N., Tonissen K.F., Krieg P.A.;
Johnson A.D., Oveenek N., Tonissen K.F., Krieg P.A.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, L26396; AAA49911.1; -.
NON TER 17
SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;
                                                                                                                                                                                                                                                                                                17 AA; 2026 MW; AEA1EB5F252E84F5 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Neural cell adhesion molecule (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence
05-JUL-2004 (TrEMBLrel. 27, Last annotation and adhesion molecule (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.v
Best Local 3; Conservative
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                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopodinae; Xenopus
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Matches 3; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   7 MIWTM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LIWIL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 MIWIM 11
                                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
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AAA49911;
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QGLEAB;
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RESULT 12 AAA49911

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RESULT 11

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Gaps

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MEDLINE-99155621; PubMed=10028295;
Dowton M., Austin A.D. of a mitochondrial rearrangement 'hot spot' in the hymenoptera.";
"Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in the hymenoptera.";
MO1. B101. Evol. 16:298-309(1999).
ENBL; AF034586; AAC79744.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
NON TER 1
SEQÜENCE 19 AA; 2291 MW; B964CCC7FDAC36C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea; Braconidae; Doryctinae; Jarra. NCBI_TaxID=64830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

38.1%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels
                                                                                                      Query Match 38.1%; Score 24; DB 2; Length 18; Best Local Similarity 62.5%; Pred. No. 2.1e+03; Matches 5; Conservative 0; Mismatches 3; Indels
EMBL, AF034603, AAC79751.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
NON TER 1
SEQÜENCE 18 AA; 2181 MW; F83846FDAEB8DCD6 CRC64;
                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome oxidase II (Fragment).
                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                       7 SLKIFMIW 14
                                                                                                                                                                           2 SLDATMIW 9
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Mitochondrion.
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Search completed: November 14, 2004, 12:07:29 Job time : 35.0426 secs

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LENGTH: 12 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-08-241-054-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                       November 14, 2004, 11:57:26; Search time 9.44681 Seconds (without alignments) 84.242 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6
Sequence 2
Sequence 5
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Sequence 3
Sequence 3
Sequence 4
Sequence 5
Sequence 5
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Sequence 3
Sequence 1
Sequence 5
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Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-241-054-51
US-08-241-054-61
US-08-390-156A-52
US-08-390-156A-61
US-08-390-156A-61
US-08-439-817-33
US-08-439-817-33
US-08-439-817-33
US-08-439-817-33
US-08-485-508-53
US-08-485-508-51
US-08-25-501-106
US-08-314-586-12
US-08-319-3185-9
US-08-319-3185-9
US-09-25-501-107
US-08-464-250-20
US-08-464-250-20
US-08-319-05-7
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-241-054-55
US-08-241-054-95
US-08-241-054-98
                                                                                                                                                                                                                                                                      478139 segs, 66318000 residues
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                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                      US-09-831-253F-3
63
1 TSLDATMIWTMM 12
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Match Length
                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 23
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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Sequence 45, Appl Sequence 58, Appl Sequence 87, Appl	Sequence 35, Appl Sequence 75, Appl Sequence 78, Appl	200, 55, 95,	44, 151, 108,	Sequence 18, Appl Sequence 81, Appl Sequence 18, Appl Sequence 61, Appl Sequence 81, Appl
1 US-08-390-156A-45 1 US-08-390-156A-58 1 HS-08-390-156A-87	1 US-08-439-817-35 1 US-08-439-817-75 1 US-08-439-817-75	1 US-08-439-817-200 1 US-08-485-508-55 1 US-08-485-508-95 1 US-08-485-508-95	1 US-09-423-823-44 4 US-09-428-0828-151 4 US-09-255-501-108	1 US-08-382-013A-18 US-08-241-054-81 1 US-08-390-156A-38 1 US-08-439-817-61 1 US-08-485-508-81
122	1222	1222	122	00000
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860	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	3 3 3 4 4 4 5 4 4 4 4 4 4 4 4 4 4 4 4 4	2 E E 4 5	4 4 4 4 4 1

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RESULT 1

US-08-210-054-50

Sequence 50, Application US/08241054

Fatent No. 56438 arrett, Ronald W. Application Stream E. Application E. Stream E. Application E. Stream E. Application E. Submand-Frisch, Beatrice Information Selecting Including Endothellum Leukocyte Adhesion TITLE OF INVENTION: Peptides and Compounds That Bind TITLE OF INVENTION: Selecting Including Endothellum Leukocyte Adhesion TITLE OF INVENTION: Selecting Including Endothellum Leukocyte Adhesion CONTRY: Alexandria Stream Stream Selecting Including Endothellum Selecting Including Endothellum Selecting Including Endothellum Selecting Including Endothellum Stream Stream Stream Stream Stream Stream E. Stream Stream Stream E. Stream E. Stream St
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Sequence 61, Application US/08241054
Patent No. 5643873
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
        7 LWTMM 11
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                                                                 RESULT 3
US-08-241-054-61
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NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                  Gaps
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                                                                                     Score 28; DB 1; Length 12;
Pred. No. 1e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: US 07/881,395
FILING DATE: US 07/881,395
FILING DATE: US 07/881,395
FILING DATE: US 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/POCKET NUMBER: 000324-002
TELEPHONE: 415-84-7400
TELEPHONE: 415-84-7400
TELEPHONE: 12 AMIGNERISELES
SEQUENCE CHARACTERISTICS:
LENGTH: 12 AMIGNERISELES
LINFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/08241054 Patent No. 5643873
                                                                                                                              4; Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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Best Local Similarity
Matches 4; Conservat
                                                                                Query Match
Best Local Similarity
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8 IWTWM 12

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PREJIGATION DATES.

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Sequence 61, Application US/08390156A
; Sequence 61, Application US/08390156A
; Patent No. 564848
; GENERAL INFORMATION:
APPLICANT: Cavila, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: BLAM-1
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                         APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
FILING DATE: 16-FEB-1996
FILING DATE: 05-MAY-1993
FILING DATE: 07-MAY-1993
FILING DATE: 05-MAY-1993
FILING DATE: 06-MAY-1992
ATTORNEY, GG-MAY-1992
ATTORNEY, AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REGISTRATION NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-WAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-WAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1023.1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Affymax Technol
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 IWTMM 12
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Pred. No. 1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens (Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
                  APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCES. Alfymax Technologies, N.V.
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Datentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,156A

PILING DATE: 16-FEB-1996

PRIOR APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION NUMBER: US 07/881,395

FILING DATE: 06-MAY-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                E: Affymax Technologies, N.V. 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFRENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/08390156A Patent No. 5648458 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 22:
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Dower, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
                                                                                                                                                   STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MIWIMM 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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Gaps

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STRANDEDNESS: single
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APPLICANT: Cwirls, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Ruhland-Fritech, Beatrice
APPLICANT: Ruhland-Fritech, Beatrice
TITLE OF INVENTION: Selecting Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
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Pred. No. 1e+02;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,817

FILING DATE: 12-MAY-1995

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US 08/241,054

FILING DATE: 11-MAY-1994

PRIOR APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION NUMBER: US 07/881,395

FILING DATE: 05-MAY-1992

ATTONIEY/AGENT INFORMATION:

ANDER CONTREY/AGENT INFORMATION:

ANDER CONTREY/AGENT INFORMATION:

ANDER CONTREY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-046/1056.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEPAS: 415-424-0832
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/08439817
Patent No. 5728802
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-032
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: alinear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0.
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amino acid
                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Affymax
STREET: 4001 Mirand
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                 8 IWTMM 12
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GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Coller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                    Query Match 44.4%; Score 28; DB 1; Length 12; Best Local Similarity 66.7%; Pred. No. 1e+02;
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                                                                                                                                                                                                                                  1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: ELEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION NUMBER: US 08/241,054
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATPONRY/AGENT INFORMATION:
NAME: ABANCH LANGATION:
NAME: AB
                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08439817 Patent No. 5728802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTY A001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
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REGISTRATION NUMBER: 36,691
REPERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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80.0%;
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STRANDEDNESS: single
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, MOLECULE TYPE: peptide US-08-439-817-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Sequence 50, Application US/08485508

Patent No. 5786322

GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Koller, Kerry J.
APPLICANT: Martens, Christine L.
APPLICANT: Martens, Christine L.
APPLICANT: Ruland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.4%; Score 28; DB 1; Length 12; 66.7%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRIER TRADABLE FORM:

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
TITING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
PILING DATE: 11-MAY-1994
CLASSIFICATION NUMBER: US 08/057,295
PILING DATE: 05-MAX-1993
PRIOR APPLICATION NUMBER: US 08/057,295
PILING DATE: 05-MAX-1993
PRIOR APPLICATION NUMBER: US 08/057,295
FILING DATE: 06-MAX-1993
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAX-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                3: Affymax Technologies, NV 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 53, Application US/08485508; Patent No. 5786322; GENERAL INFORMATION: APPLICANT: Barrett, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stevens, Lauren L. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11 'US-08-53
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                                                                                                                                                                                                                                                                                        APPLICANT: Dower, William J.
APPLICANT: Bower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Ruthand-Fritsch, Beatrice
APPLICANT: Ruthand-Fritsch, Beatrice
APPLICANT: Ruthand-Fritsch, Beatrice
APPLICANT: Selecting Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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Mismatches
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FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Affymax Technologies, NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        Sequence 41, Application US/08439817
Patent No. 5728802
GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                       Barrett, Ronald W. Cwirla, Steven E. Dower, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4001 Miranda Ave
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4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 4; Conserv
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                                          8 IWTMM 12
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                                                                              7 LWTMM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C. COUNTRY:
                                                                                                                                                                          -08-439-817-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-439-817-41
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Matches
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Gaps

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EXPRESSION VECTOR,
                                                                                              Peptides and Compounds That Bind
Selectins Including Endothelial Leukocyte Adhesion
Molecule I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
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                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: RIDAPY disk
MEDIUM TYPE: RIDAPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHILL
COMPUTER: BATCHILL
COMPUTER: BATCHILL
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/485,508
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000324-002/1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                TITLE OF INVENTION: Peptides and ComporTITLE OF INVENTION: Selectins Includit TITLE OF INVENTION: MOISCULE I NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV STREET: 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAPUT, DANIEL
FERRARA, PASCUAL
GUILLEMOT, JEAN-CLAUDE
KAGHAD, MOURAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/07920519; Patent No. 5382518; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOISON, GERARD
LARBRE, ELIZABETH
LUPKER, JOHANNES
LEPLATOIS, PASCUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RICHARD
GERARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0°
1, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SALOME, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-485-508-61
                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LWTMM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-920-519-12
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Roller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
APPLICANT: Lee, Jung
TITLE OF INVENTION: Selectine Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technolomic-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/485,508

FILING DATE: 11-MAY-1994

CLASSIFICATION NUMBER: US 08/21,054

PRIOR APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION NUMBER: US 08/057,295

FILING DATE: 05-MAY-1993

PRIOR APPLICATION NUMBER: US 07/881,395

FILING DATE: 06-MAY-1992

ATTONINY/AGENT INPORMATION:

NAMM: CANNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERNEC/POCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEPHONE: 415-496-330
TELEPAX: 415-496-300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee, Jung
Martens, Christine L
Ruhland-Fritsch, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-485-508-61
; Sequence 61, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barrett, Ronald W.
Cwirla, Steven E.
Dower, William J.
Koller, Kerry J.
                                                                                                                                                                                                                                                                                                                            ALTYMBA TECHNOL CITY: 4001 Miranda Ave. CITY: Palo Alto STATE: California COUNTRY: USD ZTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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APPLICANT:
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EXPRESSION VECTOR
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GUILLEMOT, JEAN-CLAUDE
KAGHAD, MOURAD
LOISON, GERARD
LOISON, GERARD
LOISON, GERARD
LOISON, GERARD
LOISON, GERARD
SALOME, PASCUAL
SALOME, MARK
ILAREN, PATRICK
LAUNENTION: URATE OXIDASE ACTIVITY PROTEIN,
INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESINVENTION: PRICKORGANISMS AND TRANSFORMED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.4%; Score 28; DB 1; Length 13; 55.6%; Pred. No. 1.1e+02; 1; Wismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln NPR: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,586
FLING DATE: 28-SEP-1994
  SOFTWARE: Patentin Release #1.0, Version #1.25
                                                        FILING DATE:
PRICATION: 435
PRICA PAPELCATION: 435
PRICA PAPELCATION DATA:
APPLICATION NUMBER: US 07/768,083
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: FR 89 17467
FILING DATE: 29-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DCKET NUMBER: 16781/318
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-4109
TELEPHONE: (703) 683-4109
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 12, Application US/08314586; Patent No. 5541098; GENERAL INFORMATION: APPLICANT: CAPUT, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: hydrolysis product T28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: URATE TITLE OF INVENTION: RECOM TITLE OF INVENTION: MICRO NUMBER OF SEQUENCES: 40 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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4 TDVDATWQW 12
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FOLEY & LARDNER STREET: King Street Station, Suite 500,1800 Diagonal STREET: Koad, PO Box 299 CITY: ALEXANDRIA STATE: VIRGINIA STATE: USA USA ZIP: 22313-0299
                                                                        CITY: Alexandria
STATE: Virginia
COMPTRY: USB
COMPTRY: USB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/920,519
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/659,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 1; 1
Pred. No. 1.1e+02;
1; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEPLATOIS, Pascal
APPLICANT: LEPLATOIS, Pascal
APPLICANT: PESSECUE, Bernard
APPLICANT: PESSECUE, Bernard
APPLICANT: SHIRE, David
TITLE OF INVENTION: Artificial promoter for
TITLE OF INVENTION: of proteins in yeast
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16781/276 BEDL
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION VUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)83-6-9300
TELEFA: 899149
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: Hydrolysis product T 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08086410 Patent No. 5407822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.4%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :||| |
4 TDVDATWOW 12
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TSLDATMIW 9
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PRIOR APPLICATION DATA:

APPLICATION UDATA:

APPLICATION NUMBER:

FILING DATE: 25-AFR-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REFERENCE/DOCKET NUMBER: 16781/509/BEDL

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (703)834-919

TELEFAX: (703)834-919

TELEFAX: (703)834-919

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acids

TYPE: mino acids

TYPE: mino acids

TYPE: mino acids

TOPOLOGY: linear

TOPOLOGY: linear

MOLECUE TYPE: peptide

HYPOTHETICLE: NO

IMMEDIATE SOURCE:

CLONE: Hydrolysis product T 28

US-08-314-586-12

Query Match

Best Local Similarity 55-64; Pred, No. 1.18+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps

Oy 1 TSLDATMW 9

4 TDVDATWQW 12
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Search completed: November 14, 2004, 12:08:47 Job time : 10.4468 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein
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protein
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; Search time 34.7234 Seconds	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
2004, 11:57:25	
2004,	
14,	
November	
Run on:	

(without alignments) 123.973 Million cell updates/sec

US-09-831-253F-3 63 score:

TSLDATMIWTMM 12 Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp20028:\* geneseqp2003as:\* A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003bs:\* geneseqp2004s:\*

#### SUMMARIES

	ion	7 Transform	3 Transform	Transform		3 Transform	) Transform	3 Transform	_	7 Transform	9 Transform	5 Transform	) Transform	7 Transform	1 CD66 pept	7 Cancer-re	l N-termina	Human glu	2 Trpzip pe		) Trpzip pe	6 Neuronal	8 Anti-ELAM	5 Anti-ELAM	ELAM-1	DELAM-1 bi
	Description	Aay92947	Aay93008	Aay93009	Aay93094	Aay93098	Aay92950	Aay93093	Aay93007	Aay93096	Aay92949	Aay93095	Aay93010	Aay93097	Aab88161	Adc99257	Aau05001	Aau86061	Adf69672	Aaw46010	Adf69670	Aaw69116	Aar86068	Aar86065	Aaw26904	Aaw26900
	ID	AAY92947	AAY93008	AAY93009	AAY93094	AAY93098	AAY92950	AAY93093	AAY93007	AAY93096	AAY92949	AAY93095	AAY93010	AAY93097	AAB88161	ADC99257	AAUOSOO1	AAU86061	ADF69672	AAW46010	ADF69670	AAW69116	AAR86068	AAR86065	AAW26904	AAW26900
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	Score	63	63	58	20	20	20	48	37	36.5	36.5	35	35	31.5	31	31	30	30	30	29	29	29	28	28	28	28
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AAW26865 AAW63875 AAW63886 AAW638878	AAK13972 AAR61463 AAU06698 ABJ38668 ADA89077	ADG74329 ADE67540 ADE66432 ADE7609 ADE70007	ADE67387 ADE6708 AAB8891 AAB70131 ADE70548 ADE70592
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# ALIGNMENTS

RESULT 1

Hepatotropic, antagonist, transforming growth factor betal, TGF-bl, competitive inhibition, collagen synthesis stimulation inhibitor; liver, extracellular matrix degradation inhibitor; mimetope, cirrhosis. Transforming growth factor inhibitory peptide #3. Ą AAY92947 standard; peptide; 12 (first entry) 08-NOV-2000 AAY92947; AAY92947 

Homo sapiens.

WO200031135-A1.

02-JUN-2000.

99WO-ES000375 23-NOV-1999; 98ES-00002465. 24-NOV-1998; (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Claim 4; Page 80; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of srimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

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Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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Borras Cuesta F;
                                                                                                                                                                                Transforming growth factor inhibitory peptide P55.
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                         AAY93009 standard; peptide; 12
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Pred. No. 0.00011;
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Pred. No. 0.00011;
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Conservative 0;
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Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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Borras Cuesta F;
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides ANY92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the
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Pred. No. 0.00091;
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Best Local Similarity 100.00
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
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                                                                                      Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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Pred. No. 0.03;
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Borras Cuesta F;
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Borras Cuesta P;
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those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collegen synthesis in liver cells and inhibitors of synthesis of protectorytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAV92945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or stresses of the peptides are used for treatment of liver
                                                                                                                                                                                                                                                                                                                                                                                    Hepatotropic; antagonist; transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                                                                                                          Score 50; DB 3
Pred. No. 0.03;
                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                    AAY93093 standard; peptide; 12 AA.
                                                                                         disease, specifically cirrhosis
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                                                                                                                                          79.4%;
Similarity 75.0%;
9; Conservative
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                                                                                                                    Seguence 14 AA;
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76.2%; Score 48; DB 3; Length 12; 100.0%; Pred. No. 0.058;

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition, collagen synthesis stimulation inhibitor; liver, extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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100.0%; Pred. No. 5.6;
iive 0; Mismatches (
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                                                                                                                                                                                                          AAY93007 standard; peptide; 12 AA.
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The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides ANY92945-Y93131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                           Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                           Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena {\cal J}_i Borras Cuesta {\cal F}_i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.9%; Score 36.5; DB 3; 75.0%; Pred. No. 1.7e+06; iive 0; Mismatches 0;
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                          99WO-ES000375
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Les 9; Conservative
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                                                                                        Hepatotropic, antagonist, transforming growth factor betal; TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                           Transforming growth factor inhibitory peptide P142.
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(first entry)
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                                                           The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY22945-Y9313 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or disease anacidical).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-bl) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-bl and/or its receptors. Peptides AAY92945-Y91131 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-bl to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the
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useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.
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                                                                                                                                                                                                                                                 55.6%; Score 35; DB 100.0%; Pred. No. 1.7 ive 0; Mismatches
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                                       Disclosure; Page 31; 86pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                             AAY93010 standard; peptide; 12 AA.
                                                                                                                                                                                               disease, specifically cirrhosis
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                                                                                                                                                                                                                                                                            6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                         Sequence 7 AA;
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extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatotropic, antagonist, transforming growth factor betal, TGF-bl; competitive inhibition; collagen synthesis stimulation inhibitor; liver, extracellular matrix degradation inhibitor; mimetope; cirrhosis.
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                                                                                                                                                                                               DB 3;
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                                                                                                                                                                                            55.6%; Score 35; DB 100.0%; Pred. No. 13; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93097 standard; peptide; 9 AA.
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                                                                                                                                   Sequence 12 AA;
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cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras; leptin; VBGF; vascular endothelial growth factor receptor; VBGF-R1; VBGF-R2; VBGF-R3; VBGF-R3; VBGF-R3; VBGF-R3; VBGF-R3; VBGF-R3; VBGF-R3; VBGF-R3; VBR; VBR; VBR; VBR, VBGF-R3; VBF-R3; 
                                                                                                                         Cancer-related DGI-2-binder peptide - SEQ ID 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: November 14, 2004, 12:02:06 Job time : 35.7234 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DGIB-) DGI BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2001; 2001US-0345471P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2002; 2002WO-US034021
                                                                        01-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                   Unidentified.
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                        ADC99257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 isolands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one compared. The peptides are capable of modulating activation of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of Feptimelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides and adhesion of CD66 family polypeptides to other ligands. The peptides and adhesion of CD66 family polypeptides to other ligands. The peptides and adhesion of cells or modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering adhesion to a biomaterial, for altering andiogenesis by contacting andothalial cells, tumours, for detecting inflammation, for altering endothalial cells, tumour cells or immune cells, for altering an immune response, and for altering keratinocyte proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.
                                                                                                                                                                                                                                                                                                      CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; anglogenesis.
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49.2%; Score 31; DB 4; Length 14;
Best Local Similarity (50.0%; Pred. No. 80;
Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                   AAB88161 standard; peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-2000; 2000WO-US023482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0150791P.
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                                                                                                                                                                                                                                                        CD66 peptide CD66f(11)-10.
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                                                                                                                                                 AAB88161;
                                                RESULT 14
                                                                      AAB88161
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Blume A;

Dedova O,

Brissette R, Spruyt M, , Goldstein N;

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Selecting target and target binder pairs for preparing a composition for treating cancer by mixing in a reaction vessel phage expressing biological targets and phage expressing target binders.
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                                                                                                                                                                             Claim 26; SEQ ID NO 90; 172pp; English.
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Best Local Similarity
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DAGMIWFM 12

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ADC99257 standard; peptide; 20 AA.

RESULT 15

ADC99257

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2 SLDATMIWTM 11

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 90, Appl	Sequence 441, App	Sequence 97, Appl	Sequence 61, Appl	Sequence 97, Appl	Sequence 7, Appli		Sequence 44, Appl	Sequence 41, Appl		Sequence 41, Appl		Sequence 41, Appl
ΩI	US-10-280-066-90	US-10-742-379-441	US-09-753-126-97	US-09-896-896A-61	US-10-330-697-97	US-09-836-770-7	US-09-758-128-41	US-09-758-128-44	US-09-758-426-41	US-09-758-426-44	US-09-758-198-41	US-09-758-198-44	US-09-861-661-41
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	Sequence 642, App Sequence 642, App Sequence 47789, A Sequence 439, App Sequence 685, App	101, 19131, 1841, 2023,	Sequence 2024, Ap Sequence 86, Appl Sequence 602, App Sequence 20, Appl Sequence 512, Appl	6 5 5 7 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	
US-09-861 US-09-836 US-10-195 US-10-799 US-10-176	14 US-10-062-109A-642 14 US-10-005-480A-642 9 US-09-864-761-47789 16 US-10-742-379-439 15 US-10-182-252A-685	US-10-435 US-09-864- US-10-225 US-10-283	14 US-10-283-017-2024 15 US-10-410-764-86 14 US-10-190-082-602 14 US-10-357-935-20 15 US-10-182-2528-632	2-252A-6 2-252A-1 0-708-79 0-708-50 5-109-7	US-09-840-277 US-09-813-823 US-09-821-823 5 US-10-632-38 5 US-10-645-76 5 US-10-645-76
7 16 22 22 17	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	114	7 8 5 6 7 8 6 6	00111	12222222
29 46.0 29 46.0 29 46.0 29 46.0 44.4 4.4	27 42.9 27 42.9 27 42.9 26 41.3	4444	26 41.3 26 41.3 25 39.7 25 39.7	255 255 255 255 255 255 255 255 255 255	25 25 25 39.7 25 39.7 25 39.7 25 39.7
14 15 17 18	19 22 23 33	25 25 26	2000 E 6	3 6 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 6 4 4 4 4 4 4 4 4 6 0 0 0 0 0 0 0 0 0

# ALIGNMENTS

Sequence 90, Application US/10280066; Publication No. US20030180718A1; GENERAL INFORMATION:

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APPLICANT: Pillutla, Renuka C.
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Michael
APPLICANT: Brume, Arthur J.
APPLICANT: Blume, Arthur J.
APPLICANT: Blume, Arthur J.
APPLICANT: Blume, Arthur J.
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINITIES OF INVENTION: UNMBERT SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINITIES OF INVENTION NUMBER: 60/345,471
PRIOR APPLICATION NUMBER: 60/345,471
SPRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 537
SOFTWARE: Patentin Version 3.1
SEQ ID NO 90
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE

CTHER INFORMATION: DGI-2-20R-4-E6
US-10-280-066-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Escherichia coli
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Sequence 97, Application US/09753126

Patent No. US20020127219A1

GENERAL INFORMATION:

APPLICANT: OKKELS, JENS SIGURD

APPLICANT: OKKELS, JENS SIGURD

APPLICANT: OF INVENTION: IMPROVED LYSOSOMAL ENZYMES

TITLE OF INVENTION: ACTIVATORS

FILE REFERENCE: 31-000600US

CURRENT APPLICATION NUMBER: 185/09/753,126

CURRENT FILING DATE: 2001-06-11

PRIOR PLICATION NUMBER: 60/14,652

PRIOR PLICATION NUMBER: 60/210,984

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-06-02

PRIOR PLICATION NUMBER: 60/210,984

PRIOR FILING DATE: 2000-06-02

PRIOR PLICATION NUMBER: 60/211,124

PRIOR PRIOR PLICATION NUMBER: 60/211,124

PRIOR PRIOR PLICATION NUMBER: 60/211,124

PRIOR PRIOR PLICATION NUMBER: 60/211,124
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US-09-753-126-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Sequence 441, Application US/10742379
Publication No. US20040181033A1
GENERAL INFORMATION:
APPLICANT: Han, HQ
APPLICANT: Min, Hosung
APPLICANT: Min, Hosung
TILLE REFERENCE: A-828 (US)
CURRENT APPLICATION NUMBER: US/10/742,379
CURRENT APPLICATION NUMBER: US 60/435,923
PRIOR APPLICATION NUMBER: US 60/435,923
PRIOR PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 634
SOFTWARE: Patentin version 3.2
SEQ ID NO 441
LENGTH: 22
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    ORGANISM: Artificial Sequence

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SOFTWARE: Patentin Ver. 2.1
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Sequence 97, Application No. US20040009165A1

GENERAL INFORMATION:
APPLICANT: OKKELS, JENS SIGURD
APPLICANT: JENSEN, ANNE DAM
APPLICANT: JENSEN, TORBEN
APPLICANT: JENSEN, RIKKE BOLDING
APPLICANT: JENSEN, RIKKE BOLDING
APPLICANT: JENSEN, RIKKE BOLDING
TITLE OF INVENTION: ACTIVATORS
FILE REFERENCE: 31-000600US
CURRENT APPLICATION NUMBER: US/10/330,697
CURRENT PILING DATE: 2002-12-27
FRIOR FILING DATE: 2001-06-11
FRIOR FILING DATE: 1999-12-30
FRIOR FILING DATE: 1999-12-30
FRIOR PILING DATE: 1999-12-30
FRIOR PILING DATE: 1999-12-30
FRIOR PILING DATE: 1900-01-06-11
FRIOR FILING DATE: 1900-01-06-11
FRIOR FILING DATE: 1900-01-06-11
FRIOR FILING DATE: 1900-01-06-11
FRIOR FILING DATE: 1900-01-06-11
FRIOR PILING DATE: 1900-01-06-11
FRIOR FILING DATE: 1900-01-06-11
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US-09-896-896A-61

Sequence 61. Application US/09896896A

Publication No. US20030036181A1

GENERAL INFORMATION:

APPLICANT: MAXYGEN APS

TITLE OF INVENTION: PERTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES

TITLE OF INVENTION: PERTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/09/896,896A

CURRENT FILING DATE: 2000-06-29

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-08-16

PRIOR FILING DATE: 2000-08-16

PRIOR PLILOR OWNER: DK PA 2000 01092

PRIOR PLILOR DATE: 2000-08-16

PRIOR FILING DATE: 2000-07-14

PRIOR PLILOR DATE: 2000-07-14
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Score 30; DB 9; Length 13;
Pred. No. 1.1e+02;
                                                                                 3; Mismatches
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Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                          2 SLDATMIWT 10
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1 AVNATMNWT 9
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Gaps

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Sequence 44, Application US/09758128

Sequence 44, Application US/09758128

Patent No. US20020107187A1

GENERAL INFORMATION:
APPLICANT: KINGSTON, David J.
APPLICANT: WESTBROOK, Simon L.
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: WOUDLAING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
TITLE OF INVENTION: WOUNDER: US/09/758,128
CURRENT PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: 09/194,218
PRIOR PEDICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOSTWARE: PATENTIN VET. 2.0

SOSTWARE: PATENTIN VET. 2.0
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Fatent No. US20020169116A1

Fatent No. US20020169116A1

GERREAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: KINGSTON, David J.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

CURRENT APPLICATION NUMBER: 09/194,218

FRIOR APPLICATION NUMBER: 09/194,218

FRIOR APPLICATION NUMBER: 09/194,218

FRIOR APPLICATION NUMBER: AU PN9990

FRIOR APPLICATION NUMBER: AU PN9990

FRIOR FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 9; Length 7;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
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Pred. No. 1.4e+06;
1; Mismatches 0; Indels
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           PRIOR APPLICATION NUMBER: 09/194,218
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.0%;
85.7%;
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Best Local Similarity 85...
Log 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-758-128-41
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US-09-758-426-41
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US-09-758-128-41

Sequence 41, Application US/09758128

Sequence 10. US20020107187A1

SERENT NOT US US20020107187A1

APPLICANT: KINGSTON, David J.

APPLICANT: KINGSTON, David J.

APPLICANT: WESTERCOK, Simon L.

TITLE OF INVENTION: MODULATION THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILLE REPERENCE: 015786/0214

CURRENT APPLICATION NUMBER: US/09/758,128

CURRENT PILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09836770

Sequence 7, Application US/09836770

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cochran, Andrea G.
APPLICANT: Starovasnik, Melissa A.
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.6%; Score 30; DB 15; Length 13; 55.6%; Pred. No. 1.1e+02; tive 3; Mismatches 1; Indels
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/210,984
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,497
PRIOR FILING DATE: 2000-07-11
SRQ ID NO 97
LENGTH: 13
TYPE: PRI
TYPE: PRT
CORMANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SLDATMIWT 10
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1 AVNATMNWT 9
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US-09-836-770-7
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-198-41
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Sequence 44, Application US/09758426

Patent No. US20020169116A1

Patent No. US20020169116A1

APPLICANT: KINGSTON. David J.

APPLICANT: KINGSTON. David J.

APPLICANT: WESTBROOK, Simon L.

APPLICANT: WESTBROOK, Simon L.

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

FILE REFERENCE: 016786/0214

CURRENT PELING DATE: 2001-01-12

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1996-02-05

PRIOR FILING DATE: 1996-02-05

PRIOR FILING DATE: 1996-02-05

PRIOR FILING DATE: 1996-02-05

SOFTWARE OF SEQ ID NOS: 58

SOFTWARE: PALENTIN VET. 2.0

SEQ ID NO 44

LENGTH: 7
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Sequence 41, Application US/09758198

Publication No. US20020187925A1

GENERAL INFORMATION:

APPLICANT: KINGSTON, David J.

APPLICANT: GERRATY, No. US20020187925Alman L.

APPLICANT: WESTBROOK, Simon L.

ITILE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/194,218

PRIOR PELLING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-05-22

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PALENTIN VEY: 2.0

SEQ ID NO 41

LENGTH: 7
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1; Mismatches 0; Indels
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85.7%;
                                                                                                                                                          Query Match ' 46.0%;
Best Local Similarity 85.7%;
Matches 6; Conservative
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 7
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Rat
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US-09-758-198-44

1 Sequence 44, Application US/09758198

2 Sequence 44, Application US/09758198

3 EQUENCE 44, Application US/02020187925A1

4 PUBLICATION NO. US20020187925A1

5 APPLICANT: KINGSTON, David J.

5 APPLICANT: GERRATY, No. US20020187925A1man L.

5 APPLICANT: GERRATY, No. US20020187925A1man L.

7 TITLE OF INVENTION: MODILATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

7 TITLE OF INVENTION: MODILATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS

7 TITLE OF INVENTION: DATE: LEALIER APPLICATION NUMBER: US/09/194,218

7 FILE REPERENCE: CARLIER FILING DATE: 1999-02-05

7 FRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22

7 FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990

7 FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990

7 FRIOR FILING DATE: BALLIER FILING DATE: 1996-05-22

7 FRIOR FILING DATE: BALLIER FILING DATE: 1996-05-22

7 NUMBER OF SEQ ID NOS: 58

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| Sequence 41, Application US/09861661
| Publication No. US20030045676A1
| GENERAL INFORMATION:
| APPLICANT: GERRATY, NORMAN L. |
| APPLICANT: GERRATY, NORMAN L. |
| APPLICANT: WESTERCOK, SINON L. |
| TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF |
| TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF |
| TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF |
| FILE OF INVENTION NUMBER: US/09/861,661 |
| CURRENT APPLICATION NUMBER: US/194,218 |
| PRIOR PELING DATE: 1999-02-05 |
| PRIOR FILING DATE: 1999-02-05 |
| PRIOR FILING DATE: 1996-05-22 |
| NUMBER OF SEQ ID NOS: 59 |
| SEQ ID NO 41 |
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                    Length 7;
               Score 29; DB 9;
Pred. No. 1.4e+06;
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          46.0%;
                                                                                                              Conservative
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Best Local Similarity
Query Match
Best Local Similarity
Matches 6; Conserv
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Search completed: November 14, 2004, 12:26:59 Job time: 29.3404 secs

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US-09-316-770-5
Sequence S, Application US/09836770
Publication No. US20030175799A1
GENERAL INFORMATION:
APPLICANT: Cochran, Andrea G.
APPLICANT: Statucyaenik, Melissa A.
APPLICANT: Statucyaenik, Melissa A.
TITLE OF INVENTION: HAIRPIN PEPTIDES WITH A NOVEL STRUCTURAL MOTIF AND
TITLE OF INVENTION: METHODS RELATING THERETO
FILE REPERENCE: P1875
CURRENT FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 10
SEQ ID NO S
LENGTH: 16
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                                                Gaps
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Sequence 44, Application US/09861661

Publication WO. US20030045676A1

GRENERAL INFORMATION:
APPLICANT: KINGSTON, DAVID J.
APPLICANT: GERRATY, NORMAN L.
APPLICANT: GERRATY, NORMAN L.
TITLE OF INVENTION: PETTIDES, ANTIBODIES, VACCINES & USES THEREOF
FILE REFERENCE: 054270/0135
CURRENT APPLICATION NUMBER: US/09/861,661
CURRENT PAPLICATION NUMBER: 09/194,218
PRIOR APPLICATION NUMBER: AU PN9990
PRIOR FILING DATE: 1996-05-22
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PARCENTIN VET. 2.1

SEQ ID NO 44
LENGTH: 04
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Query Match

46.0%; Score 29; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels
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Pred. No. 1.4e+06;
1; Mismatches 0; Indels
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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; ORGANISM: Rattus sp.
US-09-861-661-44
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